

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2002, 07:18:07 ; Search time 1906 Seconds

(without alignments)  
14854.986 Million cell updates/sec

Title: US-09-471-459A-6

Perfect score: 1353

Sequence: 1 atgccttgcttaatggttga.....aggaagcgacagcccttag 1353

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sy: \*  
12: gb\_un: \*  
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14: gb\_vl: \*  
15: em\_ba: \*  
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17: em\_hum: \*  
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23: em\_pat: \*  
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27: em\_sy: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_hg\_hum: \*  
31: em\_hg\_inv: \*  
32: em\_hg\_other: \*  
33: em\_hggo\_inv: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	1353	100.0	1353	6	AX030434	Sequence
2	1353	100.0	1353	6	AX235179	Sequence
3	1353	100.0	1353	6	BD002060	Phosphodi
4	1353	100.0	1353	6	BD002060	Phosphodi
5	1353	100.0	1353	6	AB038040	Homo sapi
6	1273.6	94.1	2201	6	AR141679	Sequence
7	1273.6	94.1	2201	6	AX058278	Sequence
8	1093.6	80.8	1341	6	AX030430	Sequence
9	1093.6	80.8	1341	6	BD002058	Phosphodi
10	1093.6	80.8	2399	10	AF190639	Mus muscu
11	1093.6	80.8	2725	10	MMU251859	Mus muscu
12	1093.6	80.8	2823	6	AX030435	Sequence
13	1093.6	80.8	2823	6	BD002061	Phosphodi
14	1075	79.5	1175	6	AX235181	Sequence
15	1070.4	79.5	1754	10	AB057409	Sequence
16	1021.4	75.5	1723	10	AB057411	Sequence
17	1001.2	74.0	1622	10	AB057410	Rattus no
18	803.2	59.4	2992	6	AX030436	Sequence
19	803.2	59.4	2992	6	BD002062	Phosphodi
20	803	59.3	807	6	AX030432	Sequence
21	803	59.3	807	6	BD002059	Phosphodi
22	723.8	53.5	3336	6	AR141680	Sequence
23	723.8	53.5	3336	6	AX058280	Sequence
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25	536.6	39.7	1449	10	AY007702	Mus muscu
26	517.4	38.2	2870	10	RNU77880	Rattus norv
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28	500.6	37.0	1739	6	HSPDE7A	Sequence
29	500.6	37.0	3979	9	HUMPDE7A	Homo sapien
30	500.6	37.0	3987	6	AR083648	Sequence
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32	474.8	35.1	4083	6	AX332652	Homo sapi
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40	120.2	8.9	2158	6	I22474	Sequence
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43	120.2	8.9	2647	10	RATPHOSB	L27058 Rattus norv
44	120.2	8.9	3022	10	AF202732	Rattus no
45	120.2	8.9	3133	10	RNU95748	Rattus norv

## ALIGNMENTS

RESULT 1  
AX030434  
LOCUS AX030434 1353 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 6 from Patent EP1018559.  
ACCESSION AX030434  
VERSION AX030434.1 GI:10190535  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 1353)  
Fidock, M.  
Phosphodiesterase enzymes  
Patent: EP 1018559-A 6 12-JUL-2000;  
JOURNAL PFIZER LTD (GB) ; PFIZER (US)  
PFIZER LTD (GB) ; PFIZER (US)  
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source 1, 1353  
Location/Qualifiers  
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/db\_xref="taxon:9606"

BASE COUNT	384 a	327 c	330 g	312 t
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 Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTTGTTAAATGTTGAGAGGTGGCGCAATCTTTGTTGAAACCCCGATCAGAT 60  
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 DB 61 GCCAAATGTTGTCATCTGGAGATATACGACTAAGGGGTCAGAGGGGCTTCGTCT 120  
 QY 121 GAACGCCGTGGCTCTACCATTCATTGACTTCCGCTACTTTAACAGTACAGATCTCA 180  
 DB 121 GAACGCCGTGGCTCTACCATTCATTGACTTCCGCTACTTTAACAGTACAGATCTCA 180  
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 DB 601 CTGGACATCATGCTTGACCTGCTGGCTGCTGACACACACATGTGACACCCAGGGGTG 660  
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 DB 661 AACCCGCAATTTTGTATTAATAAATAACACACATCTTGCACCAACCTATTCAGATATGCT 720  
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 DB 721 GTGCGGGAATCATCATGCGCATCTACATTTGGCATGCTTCGAGAAATCAAGCTTCTT 780  
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 DB 961 TGTGCTGACATTTGCAATCTTTAGAAATCTGGAGATGAGCAAGCGTGGAGTGAAGG 1020  
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 DB 1321 GAGAGCGAGAGCAGGAAGGCGACAGCCCTAG 1353

RESULT 2  
 AX235179 1353 bp DNA linear PAT 11-SEP-2001  
 LOCUS AX235179  
 DEFINITION Sequence 1 from Patent WO0162940.  
 ACCESSION AX235179  
 VERSION AX235179.1 GI:15593770  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 (bases 1 to 1353)  
 AUTHORS Kluxen, F.W. and Hentsch, B.  
 TITLE Phosphodiesterase type 7b.  
 JOURNAL Patent: WO 0162940-A 1 30-AUG-2001;  
 MERCK PATENT GmbH (DE)

FEATURES  
 source location/Qualifiers  
 1..1353  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

CDS  
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 /note="unnamed protein product"  
 /codon\_start=1  
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 GVNQPELIRNHLNLANLYOMSVLENHMRKSTIGLRSLRLAHLPKMTDIDQQLS  
 SLILATDINKONFLRLAHHLNKLRLIEDQKDIPIQIGFNSITVEPLFRMAHNS  
 KQMSERVICEPFRGELERKELEISPLDNOQDIPIQIGFNSITVEPLFRMAHNS  
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BASE COUNT 384 a 327 c 330 g 312 t  
 ORIGIN

Query Match 100.0%; Score 1353; DB 6; Length 1353;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTTGTTAAATGTTGAGAGGTGGCGCAATCTTTGTTGAAACCCCGATCAGAT 60  
 DB 1 ATGCTTTGTTAAATGTTGAGAGGTGGCGCAATCTTTGTTGAAACCCCGATCAGAT 60  
 QY 61 GCCAAATGTTTTCATGCTGGGAGATATACGACTAAGGGGTCAGAGGGGCTTCGTCT 120  
 DB 61 GCCAAATGTTTTCATGCTGGGAGATATACGACTAAGGGGTCAGAGGGGCTTCGTCT 120

QY	121	GAGCGCGTGGCTCTCAACCATTCATTGACTTCGCCCTACTTAAAGTACAACTACTCA	180
Db	121	GAAAGCGGTGGCTCTCTCAACCATTCATTGACTTCGCCCTACTTAAAGTACAACTACTCA	180
QY	181	GGGGAGATTGGCACAGAAAAAGTGAAGACTTTTAAAGCTTCAAAATACTTCAT	240
Db	181	GGGGAGATTGGCACAGAAAAAGTGAAGACTTTTAAAGCTTCAAAATACTTCAT	240
QY	241	GCATCAAGGCGCTTCGTGGAAATTTATACCAAGACCCCTCTGCACCTGCTGGATGAAGC	300
Db	241	GCATCAAGGCGCTTCGTGGAAATTTATACCAAGACCCCTCTGCACCTGCTGGATGAAGC	300
QY	301	TACCTTGGACAAGCAGGCAATATGCTCTCCAAAGTGGGAATGTGGATTTGACATTTTC	360
Db	301	TACCTTGGACAAGCAGGCAATATGCTCTCCAAAGTGGGAATGTGGATTTGACATTTTC	360
QY	361	TTGTTTGTGCGCTTGACAATTTGGAAGACGCGGTGAACCTGTGTGGCACCTCTCAAT	420
Db	361	TTGTTTGTGCGCTTGACAATTTGGAAGACGCGGTGAACCTGTGTGGCACCTCTCAAT	420
QY	421	ACCATGGACTCATTCCTACCATTTTCAAGTATGATATGGTGCCTTACACGATTTTATGTC	480
Db	421	ACCATGGACTCATTCACCATTTTCAAGTATGATATGGTGCCTTACACGATTTTATGTC	480
QY	481	ATGCTTCAAGAAATTTACCAAGCCAAACCCGCTATACATGCTGTGTACGACGCGAC	540
Db	481	ATGCTTCAAGAAATTTACCAAGCCAAACCCGCTATACATGCTGTGTACGACGCGAC	540
QY	541	GTCACCCAGGCAATGCACTGCTCACTGAAGAAAGCCAAAGCTTGCCAGCTTCTCAAGCT	600
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QY	601	CTGGACATCATGCTTTGGACACTGTGGCTGCGACAGCACAGATGTGGACCAACGAGGATG	660
Db	601	CTGGACATCATGCTTTGGACACTGTGGCTGCGACAGCACAGATGTGGACCAACGAGGATG	660
QY	661	AACCAAGCATTTTTGAATAAAACTAACCAACCATCTTGAACCTATATGAAATATGTCT	720
Db	661	AACCAAGCATTTTTGAATAAAACTAACCAACCATCTTGAACCTATATGAAATATGTCT	720
QY	721	GTCGCGGGAATCATCACTGGCGCATCTACAAATTTGGCATGCTTGAAATCAAGGCTCTCT	780
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QY	781	GCTCATTTGGCCAAAGGAAATGACACAGAAATTTGAACAGACGCTGGGCTCTTGATCTTG	840
Db	781	GCTCATTTGGCCAAAGGAAATGACACAGAAATTTGAACAGACGCTGGGCTCTTGATCTTG	840
QY	841	GCAACAGACATCAACAGGCGAAGATGAATTTTGTACAGATTTGAAGCTCACTCCACAT	900
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QY	901	AAAAGCTTAAGACTGAGAGATGCACAGGACCTTTATGCTTCAAGATCCCTTGAAG	960
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Db	961	TGTGCTGACATTTTGCATTCCTTGAGAAATGTGGAGATGACAGAGTGGATGAAGG	1020
QY	1021	GTCGTGTGAAGAAATTTCAAGGCAAGGTGAACCTTGAACAGAAATTTGACGTGAATCACT	1080
Db	1021	GTCGTGTGAAGAAATTTCAAGGCAAGGTGAACCTTGAACAGAAATTTGACGTGAATCACT	1080
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Db	1081	CCTCTTTGTATCAACAGAAAGATTCATCTCCTAGATATACAAATTTGTTTCATGAGCTAC	1144
QY	1141	ATGCGGAGCGCGCTTCGCGGAATGGGCCATTTTACCGGATACAGCACCTGTGCGAG	1200
Db	1141	ATGCGGAGCGCGCTTCGCGGAATGGGCCATTTTACCGGATACAGCACCTGTGCGAG	1200
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D	301	TACCTTGGACAAGAGGCATATCTCTCCAAATGGAAATGNGGATTTTGGACATTTTC	360
O	361	TTGTTTGAATCGCTTGACAAATGGAAGAAGCTGCTAACTGTGTGSCACCTCTTCAAT	420
D	361	TTGTTTGAATCGCTTGACAAATGGAAGAAGCTGCTAACTGTGTGSCACCTCTTCAAT	420
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D	421	ACCCATGGACTCATTTACCATTTTCAAGTTAGATATGCTGACCTTTACACCGATTTTATGTC	480
O	481	ATGTTTCAAGAAGATTATCCACAGCCAAACCCGATATCAATATCCTGTTCACGCAGCCGAC	540
D	481	ATGTTTCAAGAAGATTATCCACAGCCAAACCCGATATCAATATCCTGTTCACGCAGCCGAC	540
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D	541	GTCACCCGAGGCATGCACTGCTTACTTAAGAGAGCCAAAGCTTCCAGACTCTCCACAGCCT	600
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D	601	CTGGACATCATGCTTGGACCTCTGGCTGCGACACACATGATGGACCCACAGGAGGTG	660
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D	661	AACCGACCATTTTGGATTAATAAACTAAACACCATCTTSCAAACCTATATACGATATGTCT	720
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D	721	GTCGCGGAGATCATCTGCGCATCTCAACTTGGATTTGGATTTGGATTAACAAGCTTCTT	780
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D	781	GCTCATTTTGGCCAAAGGAATGATGATATTTTGGACAGATTTGAAGCTCACCTCCACAAAT	840
O	841	GCAACAGACATCAACAGGCGAATGAAATTTTGGACAGATTTGAAGCTCACCTCCACAAAT	900
D	841	GCAACAGACATCAACAGGCGAATGAAATTTTGGACAGATTTGAAGCTCACCTCCACAAAT	900
O	901	AAAGACTTAAGACTGGGAGATGACACAGACAGGCACTTTATGCTTAGATCGCTTGAAG	960
D	901	AAAGACTTAAGACTGGGAGATGACACAGACAGGCACTTTATGCTTAGATCGCTTGAAG	960
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D	961	TGTGCTGACATTTTCCATCTCTTGTAGATCTGGGAGATGTGCAAGACAGTGGATGTAAAG	1020
O	1021	GTCGTGTGAAGAAATTCACAGGCAAGGTGAACCTTGAACAGAAATTTTCAACGTGAATCACT	1080
D	1021	GTCGTGTGAAGAAATTCACAGGCAAGGTGAACCTTGAACAGAAATTTTCAACGTGAATCACT	1080
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D	1081	CCTCTTTGTATATCAACAGAAAGATTCATCCCTAGATATCAAAATTTGTTTCAATGACTCAC	1140
O	1141	ATGTGTGGAGCCGCTTCCCGGGAATGGGGCCATTTTACAGGGGTAAACAGACCCGTGTGGAG	1200
D	1141	ATGTGTGGAGCCGCTTCCCGGGAATGGGGCCATTTTACAGGGGTAAACAGACCCGTGTGGAG	1200
O	1201	AAACTGTGTGGCCACCTCGACACACAAAGGCCCATGGAAGAGCCTGTTGCCACAGCAG	1260
D	1201	AAACTGTGTGGCCACCTCGACACACAAAGGCCCATGGAAGAGCCTGTTGCCACAGCAG	1260
O	1261	CACGAAAGCAGGGGCAAGAGTGGCAGCGGGCTGTACACGACACCGCAGGCCAAGGACT	1320
D	1261	CACGAAAGCAGGGGCAAGAGTGGCAGCGGGCTGTACACGACACCGCAGGCCAAGGACT	1320
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D	1321	GAGAGCGAGAGCAGGAAGCGACAGCCCTTAG	1353

LOCUS	AB038040	RESULT 4
DEFINITION	AB038040 Homo sapiens HSPDE7B mRNA for cyclic nucleotide phosphodiesterase 7B, complete cds.	1921 bp mRNA linear PRI 09-JUN-2000
ACCESSION	AB038040.1	GI:8439496
VERSION	AB038040.1	
KEYWORDS	AB038040.1	
SOURCE	AB038040.1	
ORGANISM	AB038040.1	
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AUTHORS	AB038040.1	
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BASE COUNT	AB038040.1	
ORIGIN	AB038040.1	
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Best Local Similarity	AB038040.1	
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366	GCCAAATGTTTGCATGCTGGAGAGTATACGACATGAGGGGTGACGAGGGGTTGCTGCT	425
121	GAAGCGCGTGGCTCCATCCATTCATTCAGCTTCGGCTACTTAACAGTACACATACTCA	180
426	GAAGCGCGTGGCTCCATCCATTCATTCAGCTTCGGCTACTTAACAGTACACATACTCA	485
181	GGGAGATTGGACACCAAGAAAAAGGTGAAAGACATATTAAAGCTTCAAGATACCTTCAT	240
486	GGGAGATTGGACACCAAGAAAAAGGTGAAAGACATATTAAAGCTTCAAGATACCTTCAT	545
241	GCATCAAGCGCTGCTTGTGGAATTTTACACAGAGCCCTCGACCTGCTGATGAAGAC	300
546	GCATCAAGCGCTGCTTGTGGAATTTTACACAGAGCCCTCGACCTGCTGATGAAGAC	605

QY	301	TACCTTGGACAAAGCAAGCAATTCGCTCCACAAAGTGGGAATGGGATTTTACAAATTTTC	360
Db	606	TACCTTGGACAAAGCAAGCAATTCGCTCCACAAAGTGGGAATGGGATTTTACAAATTTTC	665
QY	361	TTGTTTGTATGCTTGACAAATGGAAACAGCCTTGCTGAACACTGTTTGGCCACTCTTCAAT	420
Db	666	TTGTTTGTATGCTTGACAAATGGAAACAGCCTTGCTGAACACTGTTTGGCCACTCTTCAAT	725
QY	421	ACCATGTGACTCATTCACCAATTTTCAAGTTTAGATATGTGTACCTTTACACGATTTTATGTC	480
Db	666	TTGTTTGTATGCTTGACAAATGGAAACAGCCTTGCTGAACACTGTTTGGCCACTCTTCAAT	725
QY	481	ATGGTTCAAGAAAGATTTCACACAGCCCAAAACCCGTATTCACAAATGCTTTTACCCAGCCGAC	540
Db	786	ATGGTTCAAGAAAGATTTCACACAGCCCAAAACCCGTATTCACAAATGCTTTTACCCAGCCGAC	845
QY	541	GTCACCCAGGCCATGCACTGCTACTGTAAGAGGCCAAAGCTTGCCAGCTTCTCCACGCT	600
Db	906	CTGGACATCATGCTTGACACGTGCTGCTGACAGCAGCACAGATGTGGACCCACCCAGGGGTG	965
QY	601	CTGGACATCATGCTTGACACGTGCTGCTGACAGCAGCACAGATGTGGACCCACCCAGGGGTG	660
Db	846	GTCACCCAGGCCATGCACTGCTACTGTAAGAGGCCAAAGCTTGCCAGCTTCTCCACGCT	905
QY	661	AACGAGCATTTTGTGATTAATAAATAACCAACACATCTTGCAAACTATATAGAAATATGCT	720
Db	966	AACGAGCATTTTGTGATTAATAAATAACCAACACATCTTGCAAACTATATAGAAATATGCT	1022
QY	721	GTCGTGAGAAATCATCTGGCATCTACAAATTTGGCATGCTTCGTGAGAAATCAAGGCTTCT	780
Db	1026	GTCGTGAGAAATCATCTGGCATCTACAAATTTGGCATGCTTCGTGAGAAATCAAGGCTTCT	1085
QY	781	GTCATTTGCGCAAGGAAATGACACAGCATTTGAACACAGTGGGCTGCTGATCTTG	840
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QY	901	AAGACATTAAAGACTGGAGATGCAACAGCACAGGCACTTTATGCTTTCAGATGCGCTTGAAG	960
Db	1206	AAGACATTAAAGACTGGAGATGCAACAGCACAGGCACTTTATGCTTTCAGATGCGCTTGAAG	1265
QY	961	TGTCCTGACATTTGCAATCCTTGTAAATCTGGGAATATGACACAGTGGAGTGAAGG	1022
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QY	1021	GTCGTGAAATAATTCACAGGCAAGGTGAACCTTGACACAGAAATTTTCACTGGAAATCACT	1080
Db	1326	GTCGTGAAATAATTCACAGGCAAGGTGAACCTTGACACAGAAATTTTCACTGGAAATCACT	1385
QY	1081	CTCTTTGTATATCAACAGAAAGATTCATCCTAGTATACAAATTTGGTTTCATGAGCTAC	1140
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QY	1261	CACGAAAGCAGGGGCAAGCACTGGCAGCGGGCTTGACCAAGCACAGCAGGCGCCAAAGGACT	1322
Db	1566	CACGAAAGCAGGGGCAAGCACTGGCAGCGGGCTTGACCAAGCACAGCAGGCGCCAAAGGACT	1622
QY	1321	GAGAGCGAGAGCAGGAAGGCGACAGGCCCTTAG	1353
Db	1626	GAGAGCGAGAGCAGGAAGGCGACAGGCCCTTAG	1658

FEATURES	source	Location/Qualifiers
LOCUS	HS4251860	2653 bp mRNA linear PRI 24-MAY-2000
DEFINITION	HS4251860	Human sapiens mRNA for camp specific phosphodiesterase 7B (PDE7B gene).
ACCESSION	AJ251860	GI:8216982
VERSION	AJ251860.1	GI:8216982
KEYWORDS	pDE7B gene; phosphodiesterase 7B.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
AUTHORS	1 (bases 1 to 2653)	
TITLE	Gardner,C., Robas,N., Cawhill,D. and Fidock,M.	
JOURNAL	Cloning and characterization of the human and mouse PDE7B, a novel	
MEDLINE	Biochem. Biophys. Res. Commun. 272 (1), 186-192 (2000)	
REFERENCE	2 (bases 1 to 2653)	
AUTHORS	Fidock,M.D.	
TITLE	Direct Submission	
JOURNAL	Submitted (14-DEC-1999) Fidock M.D., Genetic Technologies, Pfizer	
	Central Research, Ramsgate Road, Sandwich, Kent CT13 9ND, UNITED	
	KINGDOM	
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Best Local Similarity	100.0%; Prid. No. 0;	
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OY	358 GCCAAATGTTGTCATCTGGAGATATACGACTAAGGGGTCAGACGGGGTTCTGCT	417
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Db  
721 GTGCTGGAATTCATCTGCGCATCTACAAATTTGGCATGCTTGCAGAAATCAAGCTTCT 780  
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1138 GCACAGACATCAACAGGCAAGTAATTTTGTACACAGATTTGAAGCTCACCTCCACAT 1197  
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1198 AAAGACTTAAGACTGAGAGATGACACAGACAGCAGCTTATGCTAGATCCGCTTGAAG 1257  
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ARI41679 2201 bp DNA linear PAT 08-Aug-2001  
LOCUS ARI41679  
DEFINITION Sequence 2 from patent US 6146876.  
ACCESSION ARI41679  
VERSION ARI41679.1 GI:15101195  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
REFERENCE  
1. (bases 1 to 2201)  
Robison, K.E., Kapeller-Libermann, R. and White, D.  
2005, a novel human cyclic nucleotide phosphodiesterase  
TITLE  
JOURNAL  
Patent: US 6146876-A 2 14-NOV-2000.  
FEATURES  
location/Qualifiers  
source  
1..2201  
BASE COUNT 581 a 577 c 582 g 461 t  
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Query Match 94.1%; Score 1273.6; DB 6; Length 2201;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1276; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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RESULT 7  
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LOCUS AX058278 2201 bp DNA linear PAT 17 -JAN-2001  
DEFINITION Sequence 2 from Patent WO0077226.  
ACCESSION AX058278  
VERSION AX058278.1 GI:12310776  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2201)  
Robison, R.E., Kapeller-Libermann, R. and White, D.  
2002, a novel human cyclic nucleotide phosphodiesterase  
Patent: WO 0077226-A 2 21-DEC-2000;  
Millennium Pharmaceuticals, Inc. (US)  
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Best Local Similarity 99.7%; Pred. No. 0; Mismatches 4; Indels 0; Gaps 0;  
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DEFINITION	Sequence 2 from Patent Epl10559.		
ACCESSION	AX030430		
VERSION	AX030430.1	GI:10190533	
KEYWORDS			
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1341)		
TITLE	Phosphodiesterase enzymes		
JOURNAL	Patent: EP 1018535-A 2, 12 -JUL-2000;		
FEATURES	Pfizer LTD (GB); Pfizer (US)		
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Best Local Similarity	90.1%; Pred. No. 3.6e-279;		
Matches 1171; Conservative	0; Mismatches 129; Indels 0; Gaps 0;		
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Qy	121	GAAGCGGTGGCTTCATCCCATTCATTCGCTCCGCTACTACTTAACAGTACACATCTA	180
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Qy	181	GGGAGATTGGACCAAGAAAAAGGTGAAGAGCTATTAAAGCTTTCAAAGATCTTCAT	240
Db	181	GGGAGATTGGACCAAGAAAAAGGTGAAGAGCTATTAAAGTTCCAAAGATCTTCAT	240
Qy	241	GCATCAAGGCTGCTGTTGGAATTATACACAGAGCCCTGTGCACCTGTGATGAAGAC	300
Db	241	GCATCAAGGCTGCTGCGGGGAGATTATACCGAGAGCCCTGTGCACCTGTGATGAAGAC	300

	RESULT_9	LOCUS	BD002058	1341 bp	DNA	linear	PAT	31-JAN-2002
QY	301	TACCTTGGACACGACGAGCATATGCTCTCTCCAAAGTGGGAAATGTGGATTTTGGACATTTTC	360					
Db	301	TACCTTGGACACGACGAGCATATGCTCTCTCCAAAGTGGGAAATGTGGAGATTTTGGACATTTTC	360					
QY	361	TTGTTTGAATGCTTGGACAAATGGAACACGCTGGTAACTAGACTGTGTGGCCACTTCTCAAT	420					
Db	361	TTGTTTGAATGCTTGGACAAATGGAACACGCTGGTAACTAGACTGTGTGGCCACTTCTCAAC	420					
QY	421	ACCAGTAGACTCATCTACCCATTTTCAAGTTAGATATGTGACCTTACACCGATTTTATGTC	480					
Db	421	TCCACTGGGCTCATCCACCCATTTTCAAGCTCGATATAGTGGACCTTGCACAGTGTCTGGGTT	480					
QY	481	ATGCTTAAAGAAAGTATACCCACAGCCAAAACCCGTTATCTCAATGCTGTTCACGACGCCAG	540					
Db	481	ATGCTTAAAGAAAGTATACCCAGGCTCAACCCATCTCCCAATGCTGTTCACGACGCCGAC	540					
QY	541	GTCACCCAGGCGCATGCTCTCTACCTCGAAAGGCCAAAGCTTGCACAGTTTCCACGCTT	600					
Db	541	GTCACCCAGGCGCATGCTCTTACCTCGAAGGCCAAAGTGGGCAAGTTTCCACGCTT	600					
QY	601	CTGACACATCATGCTTGGACGCTGGCTGTGAGAGACACACGATGTGGACCCACCGAGGGT	660					
Db	601	CTGACACATCATGCTTGGACGCTGGCTGTGAGAGACCTCATGACGTGTGGACCCACCGAGGGT	660					
QY	661	AACCAAGCATTTTGTGATTTAAACTAACCAACCATTTTGCAAAACCTATATCAAGATATGTCT	720					
Db	661	AACCAAGCATTTTGTGATTTAAACTAACCAACCATTTTGCAAAACCTATATCAAGATATGTCT	720					
QY	721	GTGCTGAGAAATCATCATCTGGCGATCTACAAATGTGCATGCTTGCAGATCAAGGCTCTT	780					
Db	721	GTACTGGAGATATCACCACTGGCGATCTTAAATTTGGCATGCTTGCAGATATACGCTCTCTG	780					
QY	781	GCTCATTTGGCCAAAGGAAATGACACAGATATTTGAACAGCAGCTGGGCTCCCTTGAATCTTG	840					
Db	781	GCTCATTTGGCCAAAGGAAATGACACAGATATTTGAACAGCAGCTGGGCTCCCTCATCTTG	840					
QY	841	GCAACACATCTCAACAGGCGAATGAAATTTTGGACACAAATTTGAAGAGCTCACCTCCACAT	900					
Db	841	GCCACGATATATCAACAGACAGAAATGAGTTTGGACCCGCTTAAAGCTCACCTCCACAT	900					
QY	901	AAAGCAATTAAGACTGGGAGATGGACACAGGACGACGACTTATGCTTCAAGATCGGCTTGAAG	960					
Db	901	AAATATTTGAGACTGGGAGATATGACAGGACACACACTTATGCTTCAAGATCGGCTTGAAG	960					
QY	961	TGTCCTGACATTTGCAATCTCTGTGAAATTTGGAGATGAGACACAGCTGGATGTGAAGG	1020					
Db	961	TGTGTGACATTTGCAATCTCTGTGCTATCTGTGGAGATGAGACACAGCTGGATGTGAAGG	1020					
QY	1021	GTCGTGAAAGAAATTTCTACAGGCAAGGTGAATTTGAACAGAAATTTGAATCTGGAATTCAGT	1080					
Db	1021	GTCGTGAAAGAAATTTCTACAGCAAGGTGACCTTTGAACAGAAATTTGAACGTGAATTCAGT	1080					
QY	1081	CCTCTTTGTATATCAACGAAAGATTTCCATCCCTAGTATATCAAAATTTGGTTTCATGAGCTAC	1140					
Db	1081	CCTCTTTGTATATCAACAGAAAGATTTCAATCCCTACATATCAAAATTTGGTTTCATGAGCTTAC	1140					
QY	1141	ATCTGTGAGCGGCTCTCCGGGATATGGGCGCATTTTACAGGGGTAAACACACCTGTCGGAG	1200					
Db	1141	ATCTGTGAGCGCGCTGTTCCGGGAGTGGGCGCGGCTTTACTGTGGAAACACACCTGTCGGAG	1200					
QY	1201	AACATGCTGGGGCCACCTCGACACACAAACAGGCGCCGTGGAGAGACCTGTTGCCACGAGAG	1260					
Db	1201	AACATGCTGAAGCCATCTCCGGCACAACAAAGCCCAAGCTGTGAAGAGACCTGTCTCATTCAG	1260					
QY	1261	CACGAAAGCAGGGGCGACAGTGGCAGCGGGCTTGACACAG	1300					
Db	1261	CACAGACGACAGGGGCGACGCGCACGAGACCTGTGGCGGGCCCCG	1300					



DEFINITION	Phosphodiesterase enzyme.
ACCESSION	BD002058.1 GI:18628798
VERSION	BD002058.1
KEYWORDS	JP 2000197494-A/1.
SOURCE	Mus sp.
ORGANISM	Mus sp.
REFERENCE	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 1341)
TITLE	FidoKku, M.
JOURNAL	Phosphodiesterase enzyme Patent: JP 2000197494-A 1 18-JUL-2000; Pfizer INC
COMMENT	OS Mus sp. (mouse) PN JP 2000197494-A/1 PD 18-JUL-2000 PF 22-DEC-1999 JP 1999364000 PR 23-DEC-1998 GB 9828603:2.17-SEP-1999 GB 9922123:6 PR 09-NOV-1999 EP 99308902:8 PI MARK FIDOKKU PC C12N15/09,A61K31/7088,A61K38/00,A61K38/46,A61K45/00,A61K48/00, PC A61P43/00, PC A61P43/00, PC A61P43/00,C12N9/16,C12Q1/44,C12Q1/68,G01N33/15,G01N33/50, PC G01N33/575, PC C12N15/00,A61K37/02,A61K37/54 CC FH Key FT source Location/Qualifiers 1.1341 /organism='Mus sp. (mouse)'. Location/Qualifiers 1.1341 /db_xref='taxon:10095'
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Query Match	80.8%; Score 1093.6; DB 6; Length 1341;
Best Local Similarity	90.1%; Pred. No. 3.6e-279;
Matches 1171; Conservative	0; Mismatches 129; Indels 0; Gaps 0;
1	ATGCTGTGTTTAATGTTGAGAGGTGGCGAAATCTGTTGAGAACCCGATCAGAT 60
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61	GCCAAATGTTTGGATGCTGGGAATATATACATCAAGGGGTCAGACGGGGTCTGCT 120
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61	GTCAAATGTTTGGATGCTGGGAATATATACATCAAGGGGTCAGACGGGGTCTGCT 120
121	GAGCCCGTGGCTCTACCCATTCATGTGACTTCGCGCTACTTAAAGTACAACTACTCA 180
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121	GAGCCCGTGGCTCTACCCATTCATGTGACTTCGCGCTACTTAAAGTACAACTACTCA 180
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181	GGGGGATTTGGACCAAGAAAAGGTGAAAACATTAATTAAGCTTCAAGATTAATTCAT 240
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301	TACCTTGGACAAGCAAGGCAATGCTCTTCAAGTGGGAATGGGATTTGACATTTTC 360
301	TACCTTGGACAAGCAAGGCAATGCTCTTCAAGTGGGAATGGGATTTGACATTTTC 360
361	TGTTTGAATCGTTGACAAATGGGAACAGTCTGGTAATCTTGTGTACTCTTCAAC 420
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421	ACCACATGACATTCACCATTTCAAGTATATATAGTGACCTTACACCGATTTTATG 480
421	ACCACATGACATTCACCATTTCAAGTATATATAGTGACCTTACACCGATTTTATG 480
421	ACCACATGACATTCACCATTTCAAGTATATATAGTGACCTTACACCGATTTTATG 480
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[illegible]



FEATURES  
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Location/Qualifiers  
1..2725  
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BASE COUNT 705 a 703 c 617 g 700 t  
ORIGIN  
Query Match 80.8%; Score 1093.6; DB 10; Length 2725;  
Best Local Similarity 90.1%; Pred. No. 3.9e-279;  
Matches 1171; Conservative 0; Mismatches 129; Indels 0; Gaps 0;  
OY 1 AMGTCTGTTTAATGTTGAGAGGTGGCGAAATCTTGTGTTGAGACCCGATCAGAT 60  
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DB 425 ATGCTCTGTTTATGTTGAGAGGTGGCGAAATCTTGTGTTGAGACCCGATCAGAT 484  
OY 61 GCCAATGTGTTTGCATCTGGAGATATAGCACTAAGGGGTCAAGCGGGGTTCTGCT 120  
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DB 485 GTCAATGTGTTTGCATCTAGAGATATAGCACTAAGGGGTCAAGCGGGGTTCTGCT 544  
OY 121 GAAGCCCGTGGCTCTACCCATTCATTGACTTCGGCTACTTAACAGTACAACTACTCA 180  
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DB 545 GAACCCCGTGGCTCTACCCATTCATTGACTTCGGCTACTTAACAGTACAACTACTCA 604  
OY 181 GGGGATTTGGCACCAGAAAAAGTGAAGATATTAAAGTTTCAAAAGATCTTCAT 240  
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DB 605 GGGGAAATTTGGCACCAGAAAAAGTGAAGATATTAAAGTTTCAAAAGATCTTCAT 664  
OY 241 GCATCAAGGCTGCTTCTGTAATTTATACCAAGCCCTCTGCACTGCTGGATGAAGAC 300  
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DB 665 GCATCTAGGCTTCTCGGGGGGATTTATACGGAGGCCCTCTCACTGCTGGATGAAGAC 724  
OY 301 TACCTTGGACAAGCAAGCATATGCTCTCCAAAGTGGAAATGGGATTTTGCATTTTC 360  
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DB 785 TTGTTGATCGCTTGACAAATGAAGACCGCTGTATACACTTTTGCCACCTCTTCAT 844  
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OY 541 GTTACCCAGGCGCATGCTGCTGTAAGGCAAGCCCAAGCTTGCACAGCTTCTTACGCT 600  
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DB 1145 GTACTGGAATCATGCTGCTGACATCTCAATTTGSCATGCTTGCAGATTCAGAGCTCTCT 1204  
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DB 1325 AAAGATTGAGACTGAGATATGACAGCAGCAGCTTATGCTTCAGATCGCTTGAAG 1384  
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OY 1141 ATGCTGAGCCGCTCTTCCGGGATGAGGCCCATTTACAGGTTACAGCAACCTCTGCGAG 1200  
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DB 1625 AATGCTGTGGGCTACCTGCGCACACAAAGGCCAGTGGAAAGGCTGTGCCACGAG 1684  
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AX030435 2823 bp DNA Linear PAT 16-SEP-2000  
LOCUS AX030435  
DEFINITION Sequence 7 from Patent EP1018559.  
ACCESSION AX030435  
VERSION AX030435.1 GI:10190536  
KEYWORDS  
SOURCE  
Mus sp.  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 2823)  
AUTHORS Fildock,M.  
TITLE Phosphodiesterase enzymes  
JOURNAL Patent: EP 1018559-A 7 12-JUL-2000;  
PFIZER LTD (GB) ; PFIZER (US)  
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Location/Qualifiers  
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/db\_xref="taxon:10095"  
BASE COUNT 725 a 730 c 646 g 722 t  
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Query Match 80.8%; Score 1093.6; DB 6; Length 2823;  
Best Local Similarity 90.1%; Pred. No. 3.9e-279;  
Matches 1171; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

OY 1 ATGCTTTTAAATGTTGAGAGGTGTGGAAATCTTGTGTGAGAACCCCGATCAGAAAT 60  
 DB 425 ATGCTTTTAAATGTTGAGAGGTGTGGAAATCTTGTGTGAGAACCCCGATCAGAAAT 484  
 OY 61 GCCAAATGTGTTCATGCTGGGAGATATACGACTAAAGGGGTAGAGCGGGGTGCGTGC 120  
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 OY 121 GAAGCGGTGGCTCTACCTACCTATGATCTCCGCTACTTAAAGCTTAAAGATATCTTCA 180  
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OY 1081 CCTCTTTGTAATCAACAGAAAGATTCATCCCTAGTATACAAATTTGTTTCATGAGCTAC 1140  
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RESULT 13  
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 DEFINITION Phosphodiesterase enzyme.  
 ACCESSION BD002061  
 VERSION BD002061.1 GI:18628801  
 KEYWORDS JP 2000197494-A/4.  
 SOURCE Mus sp.  
 ORGANISM Mus sp.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (Bases 1 to 2823)  
 AUTHORS Fidojku,M.  
 TITLE Phosphodiesterase enzyme  
 JOURNAL Patient. JP 2000197494-A 4 18-JUL-2000;  
 PRIZER INC  
 COMMENT OS Mus sp. (mouse)  
 PN JP 2000197494-A/4  
 PD 18-JUL-2000 JP 1998364000  
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FEATURES  
 source location/Qualifiers  
 FT 1..2823 /organism='Mus sp. (mouse)'.  
 FT 1..2823 /db\_xref='taxon:10095'

BASE COUNT 725 a 730 c 646 g 722 t  
 ORIGIN

Query Match 80.8%; Score 1093.6; DB 6; Length 2823;  
 Best Local Similarity 90.1%; Pred. No.3-9e-279;  
 Matches 1171; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

OY 1 ATGCTTTTAAATGTTGAGAGGTGTGGAAATCTTGTGTGAGAACCCCGATCAGAAAT 60  
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Qy	721	GTCGTGAGAAATATATCATCGGGCATATACAAATTTGGATCGCTTCGAAATCAAGGCTTCT	780
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Qy	841	GCACAGACATCAACAGCGAGATGAATTTTGGACAGATTGAAGAGTCAACCTCCACAT	900
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Db	1325	AAAGACTTAGACATGGAGATTTGACAGGACACACCTTATCTCAATGGCCTTGAG	1384
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Db	1505	CTCTTTGTATTAACAGAAAGATTTCATCCTAGTATTAACAATTTGGTTTATGAGCTAC	1564
Qy	1141	ATGTGGAGCGCTTCCGGGAAATGGGGCCATTTACGGGTAACAGAACCTCTGCGAG	1200
Db	1565	ATGTGGAGCGCTTGTTCGGGAGTGGGGCCGGTTTACTGTGGAAACAGCACTCTGCGAG	1624
Qy	1201	AACATGCTGGGCCACCTCCGACAAACAAGGCCAGTGAAGAGCCTTTCGCCAGCAG	1260
Db	1625	AACATGCTAAGCACTCTCGCGCACAAACAAGGCCAGTGAAGAGCCTCTGTCCAAATCAG	1684
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Db	1685	CACGACGCGAGGGGACGAGCGGCCAGGACCTCGGCGGGCCCGC	11724
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LOCUS	AX235181	1175 bp	DNA
DEFINITION	Sequence 3 from Patent WO0162940.		
ACCESSION	AX235181		
VERSION	AX235181.1	GI:15593772	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. (bases 1 to 1175)		
AUTHORS	Kluxen, F.W. and Hentsch, B.		
TITLE	Phosphodiesterase type 7b		
JOURNAL	Patent: WO 0162940-A 3 30-AUG-2001;		
FEATURES	MERCK PATENT GmbH (DE)		
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BASE COUNT	345 a	281 c	275 g 270 t 4.others
ORIGIN			
Query Match	79.5%;	Score 1075;	DB 6; Length 1175;
Best Local Similarity	97.9%;	Pred. No. 3,1e-274;	
Matches 1117; Conservative	2;	Mismatches 19;	Indels 3; Gaps 3;
OY	154	CGCCTACTTACACATGACATGACGAGGAGATTGGCACCAGAAAAAGTGAAGA	213
Db	30	CGCCTACTTACACATGACATGACGAGGAGATTGGCACCAGAAAAAGTGAAGA	89
OY	214	CGATTAGCTTCAAGAACTTCCATGATGCAAGGCTGCTGGGATTTATACCA	273
Db	90	CGATTAGCTTCAAGAACTTCCATGATGCAAGGCTGCTGGGATTTATACCA	149
OY	274	GCCCTCTGCACCTGCTGATGATGAGACTACCTTGAGCAAGCAAGGCATATGCTCCAA	333
Db	150	GCCCTCTGCACCTGCTGATGATGAGACTACCTTGAGCAAGCAAGGCATATGCTCCAA	209
OY	334	GTGGAGATGTGGGATTTTGAACATTTCTGTTGATGCTTGACAAATGGAAACAGCCTG	393
Db	210	GTGGAGATGTGGGATTTTGAACATTTCTGTTGATGCTTGACAAATGGAAACAGCCTG	269
OY	394	GTAACACTGTGTGGCAGCTCTTCATATACCATGAGACTATTTACCATTTCAAGTTAGAT	453
Db	270	GTAACACTGTGTGGCAGCTCTTCATATACCATGAGACTATTTACCATTTCAAGTTAGAT	329
OY	454	ATGGTACCTTACACCGATTTTATGATGATGTTCAAGAGATTACACAGCCAAACCCG	513
Db	330	ATGGTACCTTACACCGATTTTATGATGATGTTCAAGAGATTACACAGCCAAACCCG	389
OY	514	TATCAATATGCTGTTCACGACGACCGACGATCACCAGAGCCATGACATCTGCTGAAGAAG	573
Db	390	TATCAATATGCTGTTCACGACGACCGACGATCACCAGAGCCATGACATCTGCTGAAGAAG	449
OY	574	CCAAAGCTTGACAGCTTCTCTACAGCTCTTGAGATCATGCTTGAGATGCTGCTGCAGCA	633
Db	450	CCAAAGCTTGACAGCTTCTCTCTACAGCTCTTGAGATCATGCTTGAGATGCTGCTGCAGCA	509



Db 696 CTGGACATCATCTTGGACTATTGGCTGCAGCAGCTCATGACGTGGACCCAGGGGCTG 755

QY 661 AACCAAGCATTTTGTATAAACTAACCAACATCTTGCAAACTATATCAGATATGCT 720

Db 756 AACCAAGCATTTTGTATAAACTAACCAACATCTTGCAAACTATATCAGATATGCT 815

QY 721 GTGCTGGAGAAATCATCATCTGGGCTTACAAATTTGCGATGCTTCGAGAAATCAAGGCTTCTT 780

Db 816 GTACTGGAGAAATCACCACTGGGCTTACAAATTTGCGATGCTTCGAGAAATCAAGGCTTCTT 875

QY 781 GCTCATTTCCAAAGAAATGACACAGATATTGAACACAGCTGGGCTTCCTTGATCTTG 840

Db 876 GCTCATTTCCAAAGAAATGACACAGATATTGAACACAGCTGGGCTTCCTTGATCTTG 935

QY 841 GCACAGACATCAACAGAGGAGATGATTTTGACCAATGGAAGCTCACCTCCACAT 900

Db 936 GCCACGACATCAACAGAGGAGATGATTTTGACCAATGGAAGCTCACCTCCACAT 995

QY 901 AAAGACTTAAAGCTGGAGAGTGCACAGACAGGCACTTTATGCTTCAGATCGCTTGAAG 960

Db 996 AAGGATTTGAGACTGGAATAATACAGACAGACACTTTATGCTTCAGATCGCTTGAAG 1055

QY 961 TGTGCTGACATTTGCAATCTTGTAGAAATCTGGGAGATGAGCAAGCATGAGTGAAG 1020

Db 1056 TGTGCTGACATTTGCAATCTTGTAGAAATCTGGGAGATGAGCAAGCATGAGTGAAG 1115

QY 1021 GTCTGGAAGAAATCTACAGGCAAGGTGAATTTGAACAGAAATTTGAATGGAATCAT 1080

Db 1116 GTCTGGAAGAAATCTACAGGCAAGGTGAATTTGAACAGAAATTTGAATGGAATCAT 1175

QY 1081 CCTTTTGTAAATCAACAGAAAGATTCATCCTAGTATCAAAATTTGTTTCATGAGCTAC 1140

Db 1176 CCTTTTGTAAATCAACAGAAAGATTCATCCTAGTATCAAAATTTGTTTCATGAGCTAC 1235

QY 1141 ATCGTGGAGCCGCTCTTCGGAATGAGGCCATTTTCACGGGTAAACGACACCTGTCGAG 1200

Db 1236 ATCGTGGAGCCGCTCTTCGGAATGAGGCCATTTTCACGGGTAAACGACACCTGTCGAG 1295

QY 1201 AACATGCTGGGCACTCTGCACAAACAAAGGCCAGTGGAAAGAGCTGTTGCCAGGCTAG 1260

Db 1296 AACATGCTGGGCACTCTGCACAAACAAAGGCCAGTGGAAAGAGCTGTTGCCAGGCTAG 1355

QY 1261 CACAGAGCAGGGGCGAGCAG 1280

Db 1356 CACAGAGCAGGGGCGAGCAG 1375

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2002, 07:11:01 ; Search time 209 Seconds

(without alignments)  
11114.762 Million cell updates/sec

Title: US-09-471-459A-6

Perfect score: 1353

Sequence: 1 atgtctctttaaattgttga.....aggaagcgacagcccttag 1353

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : S\_Geneseq\_032802.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353	100.0	1353	21	AAAA6651
2	1353	100.0	1353	22	AAAS13248
3	1353	100.0	1353	22	AAAT70009
4	1270.4	93.9	2202	22	AAAC87948
5	1093.6	80.8	1341	21	AAAA6649
6	1093.6	80.8	2823	21	AAAA6794
7	1075	79.5	1175	22	AAAS13249
8	803.2	59.4	2992	21	AAAA6652
9	803	59.3	807	21	AAAA6650

10	723.8	53.5	3336	22	AAAC87949	Human short phosph
11	500.6	37.0	3987	12	AAQ14629	Human GLOBLASTOMA
12	500.6	37.0	3987	17	AAAT34376	Plasmid pRM22 (ATC
13	500.6	37.0	3987	20	AAZ32240	Human GLOBLASTOMA
14	500.6	37.0	3987	21	AAA88175	PTM22 human globl
15	463.6	34.3	2731	22	AAAS26872	Human CDNA encodin
16	398.8	29.5	427	21	AAAC02769	Human secreted pro
17	341	25.2	915	22	AAAS04874	CDNA encoding nove
18	341	25.2	915	22	AAAS30202	DNA encoding rena
19	341	25.2	915	22	AAAS26944	Human CDNA encodin
20	273.4	20.2	2375	20	AAZ33601	Human breast tumou
21	218.4	16.1	12988	22	AAAS36785	Human cardiovascular
22	218.4	16.1	18036	22	AAAS36787	Human cardiovascular
23	134.4	9.9	534	22	ABA62427	Human foetal liver
24	134.4	9.9	534	22	ABA29760	Probe #8226 for ge
25	134.4	9.9	534	22	AAK10765	Human brain expres
26	134.4	9.9	534	22	AAK36641	Human bone marrow
27	134.4	9.9	534	22	AAI17496	Probe #7429 for ge
28	134.4	9.9	534	22	AAI42403	Probe #11089 used
29	132	9.8	132	22	ABA74953	Human foetal liver
30	132	9.8	132	22	ABA39642	Probe #18108 for g
31	132	9.8	132	22	AAK23450	Human brain expres
32	132	9.8	132	22	AAK49596	Human bone marrow
33	132	9.8	132	22	AAI26706	Probe #16639 for g
34	132	9.8	132	22	AAI55477	Probe #24163 used
35	120.2	8.9	2158	12	AAQ14624	Plasmid pRATPD in
36	120.2	8.9	2158	17	AAAT34372	Plasmid pRATPD (A
37	120.2	8.9	2158	20	AAZ32229	Rat dunce-like pho
38	120.2	8.9	2158	21	AAAB8164	Plasmid pRATPD 2.
39	120.2	8.9	2433	22	AAAD09336	Rat pRPD590 CDNA e
40	120.2	8.9	2647	22	AAAD09339	Rat pRPD592 CDNA e
41	120.2	8.9	3022	22	AAAD09338	Rat pRPD593 CDNA e
42	120.2	8.9	3133	22	AAAD09340	Rat pRPD74 CDNA e
43	105	7.8	1517	22	AAAF28395	Human PDE4D6 CDNA
44	105	7.8	2178	20	AAZ32279	Human dunce-like p
45	105	7.8	2178	21	AAA88214	ppDE43 human dunce

#### ALIGNMENTS

RESULT 1	AAAA6651	standard; DNA; 1353 BP.
ID	AAAA6651	
AC	AAAA6651;	
XX		
DT	25-SEP-2000	(first entry)
XX		
DE	DNA encoding a human phosphodiesterase enzyme.	
XX		
KW	Phosphodiesterase; PDE-XIV; human; enzyme; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1.1353
FT		/tag= a "phosphodiesterase"
FT		/product=
XX		
PN	EP1018559-A1.	
XX		
PD	12-JUL-2000.	
XX		
PF	09-NOV-1999;	99EP-0308902.
XX		
PR	23-DEC-1998;	98GB-0028603.
XX	17-SEP-1999;	99GB-0022123.
XX		
PA	(PF12 ) PFIZER LTD.	
XX	(PF12 ) PFIZER INC.	
PI	Fidock M;	

XX WP1: 2000-433274/38.  
 DR P-PSDB: AA93359.  
 PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
 useful for preventing diagnosing and treating diseases associated with  
 PT inappropriate PDE-XIV expression and/or activity -  
 XX  
 PS Claim 4: Page 47-48; 104pp; English.

XX The present sequence encodes a phosphodiesterase (PDE)-XIV enzyme. The  
 CC phosphodiesterase polynucleotide and polypeptide may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PDE-XIV expression. For example, the polynucleotide  
 CC be administered to treat diseases by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of PDE-XIV. They may  
 CC also be used to study the expression and function of PDE-XIV  
 CC polypeptides and their role in metabolism. The PDE-XIV polypeptides  
 CC may be used as antigens in the production of antibodies against PDE-XIV  
 CC and in assays to identify modulators (agonists and antagonists) of  
 CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and  
 CC and activity (i.e. the PDE-XIV gene and/or expression product may be  
 CC used in the preparation of a composition for the treatment of a disorder  
 CC associated with inappropriate PDE-XIV expression and/or activity and to  
 CC screen for agents that can modulate PDE-XIV expression and or activity.  
 CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for  
 CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by  
 CC enzyme linked immunosorbant assay (ELISA)).  
 XX

XX Sequence 1353 BP: 384 A; 327 C; 330 G; 312 T; 0 other:

Query Match 100.0%; Score 1353; DB 21; Length 1353;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1353: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTCTGTTAATGTTGAGAGTGTGGGAAATCTGTTTGAGAAACCCCGATCAGAAAT 60  
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 QY 61 GCCAATGTGTTTGCATCTGCGGAGATATACGATTAAGGGGTGAGAGGGGTTCTGCT 120  
 DB 61 GCCAATGTGTTTGCATCTGCGGAGATATACGATTAAGGGGTGAGAGGGGTTCTGCT 120  
 QY 121 GAACGCGTGGCTCTTACCATTCATTCAGTTCGCTTAAAGTAAATCAATCTCA 180  
 DB 121 GAACGCGTGGCTCTTACCATTCATTCAGTTCGCTTAAAGTAAATCAATCTCA 180  
 QY 181 GGGGAGATGGGACCAAGAAAGGTAAAGATATTAAAGCTTCAAAAGATCTTCAT 240  
 DB 181 GGGGAGATGGGACCAAGAAAGGTAAAGATATTAAAGCTTCAAAAGATCTTCAT 240  
 QY 241 GGATGAAGTCTGCTGCGGAAATATACCAAGCCCTTGCACCTGCGATGAAGAC 300  
 DB 241 GGATGAAGTCTGCTGCGGAAATATACCAAGCCCTTGCACCTGCGATGAAGAC 300  
 QY 301 TACCTTGGACAAGCAAGCATATCTCTCCAAAGTGGGAATGGGATTTGACATTTTC 360  
 DB 301 TACCTTGGACAAGCAAGCATATCTCTCCAAAGTGGGAATGGGATTTGACATTTTC 360  
 QY 361 TTGTTTGAATCGCTTGCAAAATGAAACAGCCTGTAAACACTGTTTGCCACCTTCAT 420  
 DB 361 TTGTTTGAATCGCTTGCAAAATGAAACAGCCTGTAAACACTGTTTGCCACCTTCAT 420  
 QY 421 ACCCATGAGTCAATCACCATTTCAGTTAGATATGTTGACCTTACACCGATTTTATGAC 480  
 DB 421 ACCCATGAGTCAATCACCATTTCAGTTAGATATGTTGACCTTACACCGATTTTATGAC 480  
 QY 481 ATGGTTCAAGAAATATACCAAGCAAGCCGATACAGAAATGCTTCAACGACGACGAC 540  
 DB 481 ATGGTTCAAGAAATATACCAAGCAAGCCGATACAGAAATGCTTCAACGACGACGAC 540  
 QY 541 GTACACCCAGGCCATGCACTGCTACCTGAAGAGCCAAAGCTTCCACAGCTTCTCAGCCT 600

DB 541 GTACACCCAGGCCATGCACTGCTACCTGAAGAGCCAAAGCTTCCACAGCTTCTCAGCCT 600  
 QY 601 CTGACATCATGCTTGATGATGCTGCTGCTGACGACGACACGATGTGACCAACCCAGGGGTG 660  
 DB 601 CTGACATCATGCTTGATGATGCTGCTGCTGACGACGACACGATGTGACCAACCCAGGGGTG 660  
 QY 661 ACCGAGCATTTTGTGATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 720  
 DB 661 ACCGAGCATTTTGTGATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 720  
 QY 721 GTGCTGAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 DB 721 GTGCTGAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
 QY 781 GCTCATTTTGCAGAAAGAAATGACACAGATATGAAACAGAGCTGCTCTGATCTTG 840  
 DB 781 GCTCATTTTGCAGAAAGAAATGACACAGATATGAAACAGAGCTGCTCTGATCTTG 840  
 QY 841 GCAACAGACATCAACAGCAGCAATGATTTTGTACCAATTTGAAAGCTTCACTCCACAT 900  
 DB 841 GCAACAGACATCAACAGCAGCAATGATTTTGTACCAATTTGAAAGCTTCACTCCACAT 900  
 QY 901 AAAGACTTAAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
 DB 901 AAAGACTTAAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
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 DB 961 TGTGCTGACATTTGCAATCTTGTAGATCTGAGATGATGATGATGATGATGATGATGATG 1020  
 QY 1021 GTCTGTAAGAAATTTACAGGCAAGTGAATCTGAAACGAAATTTGAAATGGAATTCAGT 1080  
 DB 1021 GTCTGTAAGAAATTTACAGGCAAGTGAATCTGAAACGAAATTTGAAATGGAATTCAGT 1080  
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 DB 1081 CCTCTTGTATATCAACAGAAAGATTCATCCCTAGTATATCAAAATGTTGATGATGATG 1140  
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 DB 1141 ATCTGAGAGCGCTCTCCGGAATGAGCCCATTTTCAAGGGGTATACACACCTGTCGAG 1200  
 QY 1201 AACATGCTGGGCACTCTCCACACAAGGCCAGTGAAGAGCTGTTGCCAGAG 1260  
 DB 1201 AACATGCTGGGCACTCTCCACACAAGGCCAGTGAAGAGCTGTTGCCAGAG 1260  
 QY 1261 CACAGAAGCAGGCGCAGCGATGCGAGCGGCTGACACAGCAGCGAGGSCCAAGGAGCT 1320  
 DB 1261 CACAGAAGCAGGCGCAGCGATGCGAGCGGCTGACACAGCAGCGAGGSCCAAGGAGCT 1320  
 QY 1321 GAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
 DB 1321 GAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380

RESULT 2  
 AAS13248  
 ID AAS13248 standard; cDNA; 1353 BP.

XX AAS13248;  
 AC  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX

DE Human cDNA encoding phosphodiesterase type 7B #1.

XX Human: phosphodiesterase type 7B; ss: cardiovascular disease;  
 KW asthma, allergy; inflammatory disease; immune-related disorder;  
 KW cardiovascular; antiasthmatic; antiallergic; immunosuppressive;  
 XX antiinflammatory.  
 OS Homo sapiens.  
 XX

Key	Location/Qualifiers
FT CDS	1..1353
FT FT	/tag= a
XX	/product= "Phosphodiesterase 7B #1"
PN	WO200162940-A2.
PD	30-AUG-2001.
XX	
XX	20-FEB-2001; 2001WO-EP01858.
PF	
XX	21-FEB-2000; 2000EP-0103655.
PR	
XX	(MERE ) MERCK PATENT GMBH.
PA	
XX	Kluxen F, Hentsch B;
PI	
XX	WPI: 2001-570636/64.
DR	P-PSDB: AAU08675.
XX	
XX	Phosphodiesterase 7B proteins and nucleic acids, useful for preventing, diagnosing and treating, e.g. asthma, inflammation and allergies -
PT	
XX	
PS	Claim 5; Page 34-36; 40pp; English.
XX	
CC	The invention relates to a novel human phosphodiesterase type 7B
CC	polypeptide and the nucleic acid that encodes it. The protein and nucleic
CC	acid may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate phosphodiesterase 7B (P7B) expression. For
CC	example, The protein and nucleic acid may be used to treat
CC	disorders associated with decreased expression by rectifying mutations
CC	or deletions in a patient's genome that affect the activity of P7B by
CC	expressing inactive proteins or to supplement the patients own
CC	production of P7B. The nucleic acids may be used to produce P7B
CC	polypeptides, by inserting the nucleic acids into a host cell and
CC	culturing the cell to express the protein. The nucleic acid and its
CC	complements may also be used as DNA probes in diagnostic assays to detect
CC	and quantitate the presence of similar nucleic acids in samples, and
CC	therefore which patients may be in need of restorative therapy. The P7B
CC	polypeptides may also be used as antigens in the production of
CC	antibodies against P7B and in assays to identify modulators of it's
CC	expression and activity. The anti-P7B antibodies and antagonists may
CC	also be used to down regulate expression and activity. The anti-P7B
CC	antibodies may also be used as diagnostic agents for detecting the
CC	presence of P7B in samples (e.g. by enzyme linked immunosorbent assay
CC	(ELISA). Disorders that may be prevented, diagnosed and/or treated by
CC	the above methods include, for example cardiovascular disease, asthma,
CC	allergy, inflammation, and immune-related disorders. The present
CC	sequence encodes a human phosphodiesterase 7B.
XX	
SO	Sequence 1353 BP; 384 A; 327 C; 330 G; 312 T; 0 other;
Query Match	100.0%; Score 1353; DB 22; Length 1353;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1353; Conservative	0; Mismatches 0; Indels 0; Gaps 0
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DB	1 AAGCTTTGTTTAAATGTTAGAGAGTGTGGCGAAATCTTTTGAGAAACCCGATCAGAAT 60
QY	61 GCCAATATGTTTGCATGCTGGGAGATATAGACATPAAAGGGGTGACAGCGGGGTTCTGCT 120
DB	61 GCCAATATGTTTGCATGCTGGGAGATATAGACATPAAAGGGGTGACAGCGGGGTTCTGCT 120
QY	121 GAAGCCGCTGGCTCCTACCATTCATTTAGCTTCGCGCTACTTAAACAGTACACATACTCA 180
DB	121 GAAGCCGCTGGCTCCTACCATTCATTTAGCTTCGCGCTACTTAAACAGTACACATACTCA 180
QY	181 GGGGAGATTGGACACAGAAAAAGGTAAGTAAAGTTTCAAGATTAACATTCGCAT 240
DB	181 GGGGAGATTGGACACAGAAAAAGGTAAGTAAAGTTTCAAGATTAACATTCGCAT 240
QY	241 GCATCAAGGCTGCTTGTGGAGATTATACACAAAGCCCTCTCACCTGCTGGATGAAGAC 300

Db	241	GCATCAAGGCTGCTTCGTGGATTATACACAAAGCCCTCTGCACCGTGTGATGAAGAC	300
Qy	301	TACCTTGGACAAGCAAGGCATATCTCTCCAAAGTGGAAATGSGAATTTTGACATTTTC	360
Db	301	TACCTTGGACAAGCAAGGCATATCTCTCCAAAGTGGAAATGSGAATTTTGACATTTTC	360
Qy	361	TGTGTTGATCCGCTTGACAAATAGAAAGCGCTGGTAACACTGTTGTGCCACCTCTCAAT	420
Db	361	TGTGTTGATCCGCTTGACAAATAGAAAGCGCTGGTAACACTGTTGTGCCACCTCTCAAT	420
Qy	421	ACCCATGAGACTCATTTACCATTTCAAGTTAGATATGCTGACCTTACACCGATTTTATGC	480
Db	421	ACCCATGAGACTCATTTACCATTTCAAGTTAGATATGCTGACCTTACACCGATTTTATGC	480
Qy	481	ATGGTTCAAGAAAGATATCCACAGCCAAACCCGATATACATCTCTGTCCAGCAGCCGAC	540
Db	481	ATGGTTCAAGAAAGATATCCACAGCCAAACCCGATATACATCTCTGTCCAGCAGCCGAC	540
Qy	541	GTCACCCAGGCGCATGCACTGCTACCTGAAAGAGCAAGCTTCCAGCTTCCACAGCCT	600
Db	541	GTCACCCAGGCGCATGCACTGCTACCTGAAAGAGCAAGCTTCCAGCTTCCACAGCCT	600
Qy	601	CTGGACATCATGCTTTGGACTGCTGGCTGCACAGCACAGATGTGACCAACCCAGGGGTG	660
Db	601	CTGGACATCATGCTTTGGACTGCTGGCTGCACAGCACAGATGTGACCAACCCAGGGGTG	660
Qy	661	AACCGCATTTTGTATATTAATACCAACCACTTCTGCAAACTATATATGAAATATGCT	720
Db	661	AACCGCATTTTGTATATTAATACCAACCACTTCTGCAAACTATATATGAAATATGCT	720
Qy	721	GTCGTGGAAATTCATCACTGGCGACTTACAAATTTGGCATGCTTGAGAAATCAAGGCTTCT	780
Db	721	GTCGTGGAAATTCATCACTGGCGACTTACAAATTTGGCATGCTTGAGAAATCAAGGCTTCT	780
Qy	781	GCTCATTTTCCCAAAGGAAATATACACAGATATTTGACAGCAGCTGGGCTCTTGATCTTG	840
Db	781	GCTCATTTTCCCAAAGGAAATATACACAGATATTTGAAACAGAGCTGGGCTCTTGATCTTG	840
Qy	841	GCAACAGACATCAACAGGCAAGATATTTTGGCCGATTTGAACCTCACCCGCCAAT	900
Db	841	GCAACAGACATCAACAGGCAAGATATTTTGGCCGATTTGAACCTCACCTCCACAT	900
Qy	901	AAAGACTTAAAGACTGAGAGATGCACAGACAGGCACCTTATGCTTAGATGCGCTTGAAG	960
Db	901	AAAGACTTAAAGACTGAGAGATGCACAGACAGGCACCTTATGCTTAGATGCGCTTGAAG	960
Qy	961	TGTGCTGACATTTGCAATCCTTGTAGATCTGGAGATGACCAAGCATGSGAGTAAGG	1020
Db	961	TGTGCTGACATTTGCAATCCTTGTAGATCTGGAGATGACCAAGCATGSGAGTAAGG	1020
Qy	1021	GTCGTGAAAGATTCCTACAGGCAAGTGAACCTTGAACAGAAATTTGAACCTGGAATCACT	1080
Db	1021	GTCGTGAAAGATTCCTACAGGCAAGTGAACCTTGAACAGAAATTTGAACCTGGAATCACT	1080
Qy	1081	CCTCTTTGTAATCAACAGAAAGATTCATCCTAGTATACAAATTTGTTTCATGAGACTAC	1140
Db	1081	CCTCTTTGTAATCAACAGAAAGATTCATCCTAGTATACAAATTTGTTTCATGAGACTAC	1140
Qy	1141	ATCGTGAAGCCGCTTCCGGGAAATGGGCCATTTTCACGGGTAAACAGCACCCCTGTGAG	1200
Db	1141	ATCGTGAAGCCGCTTCCGGGAAATGGGCCATTTTCACGGGTAAACAGCACCCCTGTGAG	1200
Qy	1201	AAACATGCTGGGCGCACCTTCGCACACAAAGGCCCATGTGGAAGAGCCTGTTGCCAGGCG	1260
Db	1201	AAACATGCTGGGCGCACCTTCGCACACAAAGGCCCATGTGGAAGAGCCTGTTGCCAGGCG	1260
Qy	1261	CACAGAACACAGGGCAGAGATGGCAGGCGCTGACACAGACACCCAGGCCCAAGGAACT	1320
Db	1261	CACAGAACACAGGGCAGAGATGGCAGGCGCTGACACAGACACCCAGGCCCAAGGAACT	1320
Qy	1321	GAGAGCCGAGAGACAGAAAGCGACAGCCCTAG 1353	

Db 1321 GAGAGCGAGGAGCAGAGGCGAGGCCCTAG 1353

RESULT 3  
AA170009

ID AA170009 standard; cDNA; 1921 BP.

XX AA170009;

DT 19-DEC-2001 (first entry)

DE Human type 7B phosphodiesterase, PDE7B, coding sequence.

XX Human; type 7B phosphodiesterase; PDE7B; enzyme; ss.

XX Homo sapiens.

XX JP2001238680-A.

PD 04-SEP-2001.

PF 03-MAR-2000; 2000JP-0058159.

PR 03-MAR-2000; 2000JP-0058159.

XX (TANA ) TANABE SEIYAKU CO.

XX WPI: 2001-610057/70.

DR P-PSDB; AAG78915.

XX New phosphodiesterase for use in the development of inhibitors of high

PT selectivity and drugs of low side effect -

XX Claim 5: Page 9-12; 18pp; Japanese.

CC The present sequence is the coding sequence for human type 7B

CC phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the

CC development of inhibitors of high selectivity and drugs of low side

CC effects.

XX Sequence 1921 BP; 490 A; 491 C; 459 G; 481 T; 0 other;

Query Match 100.0%; Score 1353; DB 22; Length 1921;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTTGTGTTAATGTTGAGAGGTGGGAAATCTGTTTGAGAACCCCGATGAGAT 60  
Db 306 ATGCTTGTGTTAATGTTGAGAGGTGGGAAATCTGTTTGAGAACCCCGATGAGAT 365  
QY 61 GCCAAATGTTGTCATGCTGGAGATATACGACTAAGGGGTGACAGGGGGTGGTGT 120  
Db 366 GCCAAATGTTGTCATGCTGGAGATATACGACTAAGGGGTGACAGGGGGTGGTGT 425  
QY 121 GAAGCGGTGGCTCTACCATTCATTTGATTCGCGTACTTAACAGTACATACATCTCA 180  
Db 426 GAAGCGGTGGCTCTACCATTCATTTGATTCGCGTACTTAACAGTACATACATCTCA 485  
QY 181 GGGGAGTTGGACCAAGAAAGGTGAAAGACTATTAAAGCTTCAAAAGTACTTCCAT 240  
Db 486 GGGGAGTTGGACCAAGAAAGGTGAAAGACTATTAAAGCTTCAAAAGTACTTCCAT 545  
QY 241 GCATCAAGGTGCTGCTGGAATTTATACCAAGCCCTGACACTGCTGATGAGAGC 300  
Db 546 GCATCAAGGTGCTGCTGGAATTTATACCAAGCCCTGACACTGCTGATGAGAGC 605  
QY 301 TACCTGGACAAAGGCAATGCTCTCAAGTGGAGATGGGATTTTACATTTTC 360  
Db 606 TACCTGGACAAAGGCAATGCTCTCTCAAGTGGAGATGGGATTTTACATTTTC 665  
QY 361 TTGTTGATCGCTTGACAAATGSAAGAGCTGGTAACACTGTTGTGCCACCTCTTCAT 420  
Db 666 TTGTTGATCGCTTGACAAATGSAAGAGCTGGTAACACTGTTGTGCCACCTCTTCAT 725

QY 421 ACCGATGACTCATTCACCATTTTCAAGTTAGATATGCTGATACCGATTTTATGTC 480

Db 726 ACCGATGACTCATTCACCATTTTCAAGTTAGATATGCTGATACCGATTTTATGTC 785

QY 481 ATGTTTCAAGAAATTACACAGCCCAAAACCGTATACATGCTGTTACGACCGGAC 540

Db 786 ATGTTTCAAGAAATTACACAGCCCAAAACCGTATACATGCTGTTACGACCGGAC 845

QY 541 GTCAACCCAGGCGCATGCACTGCTACCTGAAAGAGCCAAAGCTTGCCAGCTTCACGCGCT 600

Db 846 GTCAACCCAGGCGCATGCACTGCTACCTGAAAGAGCCAAAGCTTGCCAGCTTCACGCGCT 905

QY 601 CTGACATCATGCTGAGTGTGCTGAGAGCAGCAGCAGATGTGACCCAGGGGTG 660

Db 906 CTGACATCATGCTGAGTGTGCTGAGAGCAGCAGCAGATGTGACCCAGGGGTG 965

QY 661 AACGAGCCATTTTGTATTAATAAATAACCAACCATCTTGAACCTATATCAGAAATGCTCT 720

Db 966 AACGAGCCATTTTGTATTAATAAATAACCAACCATCTTGAACCTATATCAGAAATGCTCT 1025

QY 721 GTGCTGAGAGATCATCTGCGATGTACAAATGGCATGCTTGGAATCAAGGCTTCT 780

Db 1026 GTGCTGAGAGATCATCTGCGATGTACAAATGGCATGCTTGGAATCAAGGCTTCT 1085

QY 781 GCTCATTTGCCAAAGGAAATGACACAGATTTGAACACAGCTGGGCTGCTGATCTTG 840

Db 1086 GCTCATTTGCCAAAGGAAATGACACAGATTTGAACACAGCTGGGCTGCTGATCTTG 1145

QY 841 GCACACACATCAACAGGCGAGATGAATTTTGTACCATTTGAAGCTCACCTCACAT 900

Db 1146 GCACACACATCAACAGGCGAGATGAATTTTGTACCATTTGAAGCTCACCTCACAT 1205

QY 901 AAGACTTAAGACTGAGAGTGCACAGACAGGCACTTATGCTTGTAGATGCTTGAAG 960

Db 1206 AAGACTTAAGACTGAGAGTGCACAGACAGGCACTTATGCTTGTAGATGCTTGAAG 1265

QY 961 TGTGCTGACATTTTGAATCCTTGTAGATCTGGAGATGAGCAAGCATGTAAGG 1020

Db 1266 TGTGCTGACATTTTGAATCCTTGTAGATCTGGAGATGAGCAAGCATGTAAGG 1325

QY 1021 GTCGTGAAAGAAATTCACAGGCAAGGTGAACCTGAAACAGAAATTTGAATGAAATTCAGT 1080

Db 1326 GTCGTGAAAGAAATTCACAGGCAAGGTGAACCTGAAACAGAAATTTGAATGAAATTCAGT 1385

QY 1081 CCTCTTGTATATCAACAGAAAGATTCATCCTAGATATCAAAATGGTTTCATGAGCTAC 1140

Db 1386 CCTCTTGTATATCAACAGAAAGATTCATCCTAGATATCAAAATGGTTTCATGAGCTAC 1445

QY 1141 ATCGTGAAGCGCTCTTCCGGGAATGGGCCATTTTACAGGGGTAAACAGCAACCTGTGCGAG 1200

Db 1446 ATCGTGAAGCGCTCTTCCGGGAATGGGCCATTTTACAGGGGTAAACAGCAACCTGTGCGAG 1505

QY 1201 AACATGCTGGGCACTCGACACACAAAGGCCAGTGTGAAGAGCTTGGCCAGGAG 1260

Db 1506 AACATGCTGGGCACTCGACACACAAAGGCCAGTGTGAAGAGCTTGGCCAGGAG 1565

QY 1261 CACAGAAGCGAGGGGACAGATGGGCGGCGTGAACAGACAGCAGCGAGGCAAGGAGCT 1320

Db 1366 CACAGAAGCGAGGGGACAGATGGGCGGCGTGAACAGACAGCAGCGAGGCAAGGAGCT 1625

QY 1321 GAGAGCGAGGAGGAGGAAGGCGAGAGCCCTAG 1353

Db 1626 GAGAGCGAGGAGGAGGAAGGCGAGAGCCCTAG 1658

RESULT 4

AAc87948

ID AAc87948 standard; cDNA; 2202 BP.

XX AAc87948;

DT 06-MAR-2001 (first entry)

XX Human long phosphodiesterase encoding cDNA SEQ ID NO:2.  
 DE XX  
 KW Human; long phosphodiesterase; short phosphodiesterase; diagnosis;  
 KW cyclic nucleotide phosphodiesterase; noctropic; cardiant; hypotensive;  
 KW nephrotropic; antidepressant; antinflammatory; immunosuppressive;  
 KW antifertility; antiasthmatic; vasotropic; gene therapy; dementia;  
 KW amnesia; congestive heart failure; thrombosis; pulmonary hypertension;  
 KW glomerulonephritis; bipolar depression; bronchial asthma; salt retention;  
 KW atopic disease; autoimmune encephalomyelitis; organ transplantation;  
 KW nephrotic syndrome; erectile dysfunction; ss.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 224..1732  
 FT /tag= a  
 FT /product= "long phosphodiesterase"  
 FT /note= "cyclic nucleotide phosphodiesterase"  
 PN US6146876-A.  
 PD 14-NOV-2000.  
 PF 11-JUN-1999; 99US-0330970.  
 PR 26-MAR-1999; 99US-0277423.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 PI Kapeller-Libermann R, White D, Robison KE;  
 DR MPI: 2001-023577/03.  
 DR P-PSDB: AAB36503.  
 XX  
 XX  
 PT polynucleotide encoding novel cyclic nucleotide phosphodiesterase  
 PT useful for treating disorders related with to protein e.g. dementia,  
 PT hypertension, glomerulonephritis, and organ transplantation -  
 PS Claim 1; Fig 1; 42pp; English.  
 XX  
 XX The present sequence encodes the human long phosphodiesterase which is  
 CC a cyclic nucleotide phosphodiesterase (I). (I) can have noctropic,  
 CC cardiant, hypotensive, nephrotropic, antidepressant, antinflammatory,  
 CC immunosuppressive, antifertility, antiasthmatic and vasotropic  
 CC activities, and can be used in gene therapy. (I) can be used for  
 CC treating various disorders associated or mediated by (I), such as  
 CC dementia, amnesia, congestive heart failure, thrombosis, pulmonary  
 CC hypertension, glomerulonephritis, bipolar depression, bronchial asthma,  
 CC atopic diseases, autoimmune encephalomyelitis, organ transplantation,  
 CC salt retention in nephrotic syndrome and erectile dysfunction.  
 XX  
 SQ Sequence 2202 BP; 583 A; 576 C; 582 G; 461 T; 0 other;  
 Query Match 93.9%; Score 1270.4; DB 22; Length 2202;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1274; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 314 CAAGCATATGCTCTCCAAAGTGGAAATGGGATTTTGACATTTCTTGTGATCGCT 373  
 |||||  
 Db 693 CAAGCATATGCTCTCCAAAGTGGAAATGGGATTTTGACATTTCTTGTGATCGCT 752  
 QY 374 TGACAAATGGAAACACCGCTGTGAACACTGTGTGCCACCTCTTCAATACCATGACCTCA 433  
 |||||  
 Db 753 TGACAAATGGAAACACCGCTGTGAACACTGTGTGCCACCTCTTCAATACCATGACCTCA 812  
 QY 434 TTACCATTTCAAGTTAGATATGATGATCTTACACCGATTTTATGATATGTTCAAGAAG 493  
 |||||  
 Db 813 TTACCATTTCAAGTTAGATATGATGATCTTACACCGATTTTATGATATGTTCAAGAAG 872  
 QY 494 ATTACACAGCCAAACCCGATATCACATGCTGTTCAGCAGACGAGCTACCCAGGCCA 553  
 |||||  
 Db 873 ATTACACAGCCAAACCCGATATCACATGCTGTTCAGCAGACGAGCTACCCAGGCCA 932  
 QY 554 TGCACGTCTACCTGAAAGAGCCAAAGCTTGCCAGCTTCTCAGCCCTGTGACATCATGC 613  
 |||||  
 Db 933 TGCACGTCTACCTGAAAGAGCCAAAGCTTGCCAGCTTCTCAGCCCTGTGACATCATGC 992  
 QY 614 TTGACATGCTGCTGCGTGCAGACACACGATGTGACCCACCGAGGCTGAACACCATTTT 673  
 |||||  
 Db 993 TTGACATGCTGCTGCGTGCAGACACACGATGTGACCCACCGAGGCTGAACACCATTTT 1052  
 QY 674 TGATAAAACTAACACACATCTTGCAAACTATATGATATGATGTGTGTGAGAAATC 733  
 |||||  
 Db 1053 TGATAAAACTAACACACATCTTGCAAACTATATGATATGATGTGTGTGAGAAATC 1112  
 QY 734 ATCACTGGCGATCTACAAATTTGGCATCTTGCAGAAATCAAGCTCTTGTCTATTTGCCAA 793  
 |||||  
 Db 1113 ATCACTGGCGATCTACAAATTTGGCATCTTGCAGAAATCAAGCTCTTGTCTATTTGCCAA 1172  
 QY 794 AGGAAATGACACAGATATTTGAACACAGCTGGGCTCTTGATCTTTGGCAACAGATCA 853  
 |||||  
 Db 1173 AGGAAATGACACAGATATTTGAACACAGCTGGGCTCTTGATCTTTGGCAACAGATCA 1232  
 QY 854 ACAGGAGATGATATTTTGGACAGATTTGAACCTCAACCTCCCAATTAAGACTTTAAGAC 913  
 |||||  
 Db 1233 ACAGGAGATGATATTTTGGACAGATTTGAACCTCAACCTCCCAATTAAGACTTTAAGAC 1292  
 QY 914 TGGAGATGACACAGACAGGACACTTATGCTTCATGATCGCTTGAAGTGTGACATTT 973  
 |||||  
 Db 1293 TGGAGATGACACAGACAGGACACTTATGCTTCATGATCGCTTGAAGTGTGACATTT 1352  
 QY 974 GCATCTCTTGTAGATCTGGGAGATGACAGACAGTGTGAGTGAAGGCTGTGGAAGAT 1033  
 |||||  
 Db 1353 GCATCTCTTGTAGATCTGGGAGATGACAGACAGTGTGAGTGAAGGCTGTGGAAGAT 1412  
 QY 1034 TCTACAGGCAAGGTGAACCTTGAACAAATTTGAACCTGGAATCACTCCCTTTGTAATC 1093  
 |||||  
 Db 1413 TCTACAGGCAAGGTGAACCTTGAACAAATTTGAACCTGGAATCACTCCCTTTGTAATC 1472  
 QY 1094 AACAGAAAGATTCATCCCTAGTATACAAATTTGTTTCATGAGCTACATGTTGAGCCGC 1153  
 |||||  
 Db 1473 AACAGAAAGATTCATCCCTAGTATACAAATTTGTTTCATGAGCTACATGTTGAGCCGC 1532  
 QY 1154 TCTTCCGGGAGATGGCCCATTTTCACGGGTAAACAGCACCTGTGTGGGAACATGCTGGGCC 1213  
 |||||  
 Db 1533 TCTTCCGGGAGATGGCCCATTTTCACGGGTAAACAGCACCTGTGTGGGAACATGCTGGGCC 1592  
 QY 1214 ACCTGACACAAACAAAGGCGCAATGGAAGAGCTGTGGCCAGGCGACAGAAAGCAGGG 1273  
 |||||  
 Db 1593 ACCTGACACAAACAAAGGCGCAATGGAAGAGCTGTGGCCAGGCGACAGAAAGCAGGG 1652  
 QY 1274 GCAGCAGTGGCAGCGGCGCTGACACACAGCAGCAGAGGCCAAGGAGCTGAGAGGAGAGC 1333  
 |||||  
 Db 1653 GCAGCAGTGGCAGCGGCGCTGACACACAGCAGCAGAGGCCAAGGAGCTGAGAGGAGAGC 1712  
 QY 1334 AGGAGGCGACAGCCCTTAG 1353  
 |||||  
 Db 1713 AGGAGGCGACAGCCCTTAG 1732

```
RESULT 5
AAA46649 standard; DNA; 1341 BP.
XX
XX AAA46649;
XX
XX 25-SEP-2000 (first entry)
XX
XX DNA encoding a murine phosphodiesterase enzyme.
XX
XX Phosphodiesterase; PDE-XIV; murine; enzyme; ss.
XX
XX Mus sp.
XX
XX Key 1.1341 location/Qualifiers
XX CDS /*tag= a
XX /product= "phosphodiesterase"
XX
XX EP1018559-A1.
XX
XX 12-JUL-2000.
XX
XX 09-NOV-1999; 99EP-0308902.
XX
XX 23-DEC-1998; 98GB-0028603.
XX
XX 17-SEP-1999; 99GB-0022123.
XX
XX (PE1Z ) PFIZER LTD.
XX (PE1Z ) PFIZER INC.
XX
XX Fldock M:
XX
XX WPI: 2000-433274/38.
XX
XX P-PSDB; AAY93567.
XX
XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
XX useful for preventing diagnosing and treating diseases associated with
XX inappropriate PDE-XIV expression and/or activity -
XX
XX Claim 4; Page 42; 104pp; English.
XX
XX The present sequence encodes a phosphodiesterase (PDE)-XIV enzyme. The
XX phosphodiesterase polynucleotide and polypeptide may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate PDE-XIV expression. For example, the polynucleotide
XX be administered to treat diseases by rectifying mutations or deletions
XX in a patient's genome that affect the activity of PDE-XIV. They may
XX also be used to study the expression and function of PDE-XIV
XX polypeptides and their role in metabolism. The PDE-XIV polypeptides
XX may be used as antigens in the production of antibodies against PDE-XIV
XX and in assays to identify modulators (agonists and antagonists) of
XX PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
XX PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
XX and activity (i.e. the PDE-XIV gene and/or expression product may be
XX used in the preparation of a composition for the treatment of a disorder
XX associated with inappropriate PDE-XIV expression and/or activity and to
XX screen for agents that can modulate PDE-XIV expression and/or activity.
XX The anti-PDE-XIV antibodies may also be used as diagnostic agents for
XX detecting the presence of PDE-XIV polypeptides in samples (e.g. by
XX enzyme linked immunosorbant assay (ELISA)).
XX
XX Sequence 1341 BP; 356 A; 344 C; 328 G; 313 T; 0 other:
XX
XX Query Match 80.8%; Score 1093.6; DB 21; Length 1341;
XX Best Local Similarity 90.1%; Pred. No. 0;
XX Matches 1171; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
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```
QY 61 GCCAAATGTGTTGTCATGCTGGAGATATACGACTAAGGGGTCAGACGGGGTCTGCT 120
DB 61 GTCAAAATGTGTTGTCATGCTGGAGATATACGACTAAGGGGTCAGACGGGGTCTGCT 120
QY 121 GAACGCCGTGGCTCCCTACCCATTCATTGACTCCGCTACTTAACAGTACAACTACTCA 180
DB 121 GAACGCCGTGGCTCCCTACCCATTCATTGACTCCGCTACTTAACAGTACAACTACTCA 180
QY 181 GGGAGATTGGACCAAAAGGTAAGAAAAAGTAAATATAGCTTCAAAAGATCTTCAT 240
DB 181 GGGAGATTGGACCAAAAGGTAAGAAAAAGTAAATATAGCTTCAAAAGATCTTCAT 240
QY 241 GCATCAAGGCTCTCTGCTGGAATATATACCAAGCCCTGACCTGGTGGTGAAGAC 300
DB 241 GCATCAAGGCTCTCTGCTGGAATATATACCAAGCCCTGACCTGGTGGTGAAGAC 300
QY 301 TACCTTGGACAAAGCAAGGCAATATGCTCCAAATGGGAATGGGATTTGACATTTTC 360
DB 301 TACCTTGGACAAAGCAAGGCAATATGCTCCAAATGGGAATGGGATTTGACATTTTC 360
QY 361 TTGTTGATCGCTTGACAAATGGAACAGCCTGTAACACTGTTGGCACTCTTCAAT 420
DB 361 TTGTTGATCGCTTGACAAATGGAACAGCCTGTAACACTGTTGGCACTCTTCAAT 420
QY 421 ACCCATGACATCATTCACCATTTCAAGTTAGATATGCTGACCTTACACCGATTTTATGTC 480
DB 421 ACCCATGACATCATTCACCATTTCAAGTTAGATATGCTGACCTTACACCGATTTTATGTC 480
QY 481 ATGTTCAAGAGATTATACACAGCCAAACCCGATATCAATGCTGTTCAGCAGCCGAC 540
DB 481 ATGTTCAAGAGATTATACACAGCCAAACCCGATATCAATGCTGTTCAGCAGCCGAC 540
QY 541 GTACACCAAGCCATGCTACTGCTAAGAGAGCAAGCTTCCAGCTTCCACGCT 600
DB 541 GTACACCAAGCCATGCTACTGCTAAGAGAGCAAGCTTCCAGCTTCCACGCT 600
QY 601 CTGGACATCATGCTTGGAGCTGCTGCTGAGCAGCAACAGATGTGGACACCCAGGGGTG 660
DB 601 CTGGACATCATGCTTGGAGCTGCTGCTGAGCAGCAACAGATGTGGACACCCAGGGGTG 660
QY 661 AACGACCATTTTGTATATAAATACACACCATCTTGCACCACTGTATACGAATATGCT 720
DB 661 AACGACCATTTTGTATATAAATACACACCATCTTGCACCACTGTATACGAATATGCT 720
QY 721 GTCTGGAGATCATCATCTGCGATCTTACAAATTTGGCATGCTTGGACAAATCAAGCTTCT 780
DB 721 GTCTGGAGATCATCATCTGCGATCTTACAAATTTGGCATGCTTGGACAAATCAAGCTTCT 780
QY 781 GCTCATTTGCCAAAGAAATGACACAGATATTTGACAGCAGTGGGCTCTTGTATCTTG 840
DB 781 GCTCATTTGCCAAAGAAATGACACAGATATTTGACAGCAGTGGGCTCTTGTATCTTG 840
QY 841 GCACAGATCATACAGAGCAGAGATATTTTGTACCAAGTGAACCTGACCTCCACAT 900
DB 841 GCACAGATCATACAGAGCAGAGATATTTTGTACCAAGTGAACCTGACCTCCACAT 900
QY 901 AAAGACTTAAAGCTGAGATGACAGAGAGAGAGCTTATGCTTGCATGAGATGCGCTTGAAG 960
DB 901 AAAGACTTAAAGCTGAGATGACAGAGAGAGAGCTTATGCTTGCATGAGATGCGCTTGAAG 960
QY 961 TGTGCTGACATTTGCAATCTTGTGATGCTGGAGATGAGCAAGATGGAGATGAAG 1020
DB 961 TGTGCTGACATTTGCAATCTTGTGATGCTGGAGATGAGCAAGATGGAGATGAAG 1020
QY 1021 GTCTGTGAAGAAATTTACAGGCAAGGTGAACCTTGAACAGAAATTTGACTGGAATCAAT 1080
DB 1021 GTCTGTGAAGAAATTTACAGGCAAGGTGAACCTTGAACAGAAATTTGACTGGAATCAAT 1080
QY 1081 CCTCTTGTATCAACAGAAAGATTTCCATCCTAGTATACAAATTTGTTTCAATGAGCTAC 1140
DB 1081 CCTCTTGTATCAACAGAAAGATTTCCATCCTAGTATACAAATTTGTTTCAATGAGCTAC 1140
QY 1141 ATGCTGAGAGCCGCTCTCGGGAATGGGCCATTTTACGGGTAACAGCACCCGTGCGAG 1200
```

Db 1141 ATCTGTGAGCCCTGTTCCGGAGTGGGCCCGGTTTACGTGGAACGACCCGTGCGAG 1200  
 QY 1201 AACATGCTGGGACCTCTCCACACACAGCCCAATGGAAGAGCTGTGGCCAGGCGAG 1260  
 Db 1201 AACATGCTGAGCCTCTCCGACACAAAGCCCACTGGAAGAGCTGTGTCACATCAG 1260  
 QY 1261 CACAGAGCAGGGGAGCAGTGGCAGCGGCTGACCAAG 1300  
 Db 1261 CACAGAGCAGGGGAGCAGCGGCTGACCAAGCTGCGGCGCCCG 1300

RESULT 6  
 AAA46794  
 ID AAA46794 standard: cDNA; 2823 BP.

AC AAA46794;

DT 25-SEP-2000 (first entry)

DE cDNA of a murine phosphodiesterase gene.

KW Phosphodiesterase; PDE-XIV; murine; enzyme; ss.

OS Mus sp.

PN EP1018559-A1.

PD 12-JUL-2000.

PF 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PFIZ ) PFIZER LTD.

PA (PFIZ ) PFIZER INC.

PI F1dock M;

DR WPI: 2000-433274/38.

PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosis and treating diseases associated with inappropriate PDE-XIV expression and/or activity.

PS Example: Page 48-49; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV cDNA. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).

CC Sequence 2823 BP; 725 A; 730 C; 646 G; 722 T; 0 other;

Query Match 80.8%; Score 1093.6; DB 21; Length 2823;  
 Best Local Similarity 90.1%; Pred. No. 0;  
 Matches 1171; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 1 ATGCTGTTTATGTTGAGAGTGTGCGAATCTGTTGAGAACCCGATCAGAT 60  
 Db 425 ATGCTGTTTATGTTGAGAGTGTGCGAAGTCTTGTGAGAGCCCTTAACAGAT 484  
 QY 61 GCCAATGTTGTTGATGCTGGAGATATAGCACTAAGGGGTCAGAGGGGTTGCT 120  
 Db 485 GTCAATGTTGTTGATGCTGGAGATATAGCACTAAGGGGTCAGAGGGGTTGCT 544  
 QY 121 GAACGCGGTGCTCTACCCATTGACTTCCGCTTACTTAACAGTACCAATCTA 180  
 Db 545 GAACGCGGTGCTCTACCCATTGACTTCCGCTTACTTAACAGTACCAATCTA 604  
 QY 181 GGGGAGATTGGACCAAGAAAAGTGAATAATATTAGCTTCAAGATCTTCAT 240  
 Db 605 GGGGAGATTGGACCAAGAAAAGTGAATAATATTAGCTTCAAGATCTTCAT 664  
 QY 241 GCATCAAGGCTGCTCTGTTGAAATATATACCAAGCCCTCTGACCTGCTGATGAG 300  
 Db 665 GCATCAAGGCTCTCTGCGGGGATATATACCGAGCCCTCTGACCTGCTGATGAG 724  
 QY 301 TACCTTGGACAAAGCAAGCATATGCTCTCCAAAGTGGAAATGGGATTTGACAT 360  
 Db 725 TACCTTGGACAAAGCAAGCATATGCTCTCCAAAGTGGAAATGGGATTTGACAT 784  
 QY 361 TTGTTGATGCTGTGACAAATGTAACAGCCTGTGACACCTGTGTCACCTTCAT 420  
 Db 785 TTGTTGATGCTGTGACAAATGTAACAGCCTGTGACACCTGTGTCACCTTCAT 844  
 QY 421 ACCCATGACATATCACCATTTCAGATATGTTAGTACCTTACACCATTTTATGTC 480  
 Db 845 TCCCATGGGCTCATCCACATTTTCAGATATGTTAGTACCTTTCACAGGTTTCTG 904  
 QY 481 ATGTTCAAGAAATATACCAAGCAAAACCGTATCACAATGCTGTTACAGCAGCG 540  
 Db 905 ATGTTCAAGAAATATACCAAGCAAAACCGTATCACAATGCTGTTACAGCAGCG 964  
 QY 541 GTACCCAGGCGATGACGCTACCTGGAAGAGCCAAAGCTTCCAGCTTCCAGCGCT 600  
 Db 965 GTACCCAGGCGATGACGCTACCTGGAAGAGCCAAAGCTTCCAGCTTCCAGCGCT 1024  
 QY 601 CTGACATATGCTTGGAGTGTGCTGCTGAGAGCAGACAGTGTGACACCAAGGGGTG 660  
 Db 1025 CTGACATATGCTTGGAGTGTGCTGCTGAGAGCAGACAGTGTGACACCAAGGGGTG 1084  
 QY 661 AACCAAGCAATTTTGTATATAAACTAACACCATCTTGAACCTATATCAGAAATGCT 720  
 Db 1085 AACCAAGCAATTTTGTATATAAACTAACACCATCTTGAACCTATATCAGAAATGCT 1144  
 QY 721 GTGCTGGAATATCATGAGGATCTACAAATGGATGCTGGAATATGAGGCTTCT 780  
 Db 1145 GTGCTGGAATATCATGAGGATCTACAAATGGATGCTGGAATATGAGGCTTCT 1204  
 QY 781 GCTCATTTTCCAAAGGAATGACAGATATGGAACAGCAGCTGGGCTCTGATCTTG 840  
 Db 1205 GCTCATTTTCCAAAGGAATGACAGATATGGAACAGCAGCTGGGCTCTGATCTTG 1264  
 QY 841 GCAACAGACATCAACAGCAGAAATGTAATTTTACCAAGATGAAAGCTCACCACAAT 900  
 Db 1265 GCAACAGACATCAACAGCAGAAATGTAATTTTACCAAGATGAAAGCTCACCACAAT 1324  
 QY 901 AAGAGCTTAAGCTGAGATGACAGAGCAAGCACTTATGCTCAAGTGGCTTGAG 960  
 Db 1325 AAGAGCTTAAGCTGAGATGACAGAGCAAGCACTTATGCTCAAGTGGCTTGAG 1384  
 QY 961 TGTGCTGACATTTGCAATCTTGTAGAACTGTGGAGATGAGCAAGCTGAGTAAAG 1020  
 Db 1385 TGTGCTGACATTTGCAATCTTGTAGAACTGTGGAGATGAGCAAGCTGAGTAAAG 1444  
 QY 1021 GTCTGGAAGATTTTACAGGAGTGAAGTGAACAGAAATTTGAATGGAATCACT 1080  
 Db 1445 GTCTGGAAGATTTTACAGGAGTGAAGTGAACAGAAATTTGAATGGAATCACT 1504

QY 1081 CCTCTTGTAAATCAACAGAAAGATTTCATCCCTAGTATACAAATGTTTCATGAGCTAC 1140  
DB 1505 CCTCTTGTAAATCAACAGAAAGATTTCATCCCTAGTATACAAATGTTTCATGAGCTAC 1564  
QY 1141 ATCGTGAAGCCGCTCTTCCGGGAATGAGCCCATTTACAGGGTAAACAGACCCCTGTCGAG 1200  
DB 1565 ATCGTGAAGCCGCTCTTCCGGGAATGAGCCCATTTACAGGGTAAACAGACCCCTGTCGAG 1624  
QY 1201 AACATGCTGGGCCACCTCTCGACACAAAGAGCCAGTGAAGAGCCTGTTGCCAGGACG 1260  
DB 1625 AACATGCTGAAGCATCTCGCCGACAAAGAGCCAGTGAAGAGCCTGTTGCCAATCAG 1684  
QY 1261 CACAGAGCAGGGGCGAGCAGTGGCAGGGGCGCTGACACAG 1300  
DB 1685 CACAGAGCAGGGGCGAGCAGTGGCAGGGGCGCTGACACAG 1724

RESULT 7

AA513249  
ID AA513249 standard; cDNA; 1175 BP.

XX AA513249;

XX 18-DEC-2001 (first entry)

XX Human cDNA encoding partial phosphodiesterase type 7B #2.

XX Human; phosphodiesterase type 7B; ss; cardiovascular disease;

XX asthma; allergy; inflammatory disease; immune-related disorder;

XX cardiovascular; antiallergic; antiallergic; immunosuppressive;

XX antiinflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 3..1175

XX /tag= a

XX /product= "Phosphodiesterase 7B #1"

XX /partial

XX /note= "No stop or start codon"

XX /transl\_except= (Pos:564..566,aa,Xaa)

XX /transl\_except= (Pos:1161..1163,aa:Xaa)

XX /note= "Xaa= unknown"

XX MO200162940-A2.

XX PD 30-AUG-2001.

XX PF 20-FEB-2001; 2001WO-EP01858.

XX PR 21-FEB-2000; 2000EP-0103655.

XX PA (MERCK ) MERCK PATENT GMBH.

XX PI Kluxen F, Hentsch B;

XX DR WPI: 2001-570636/64.

XX P-PSDB: AAU08676.

XX Phosphodiesterase 7B proteins and nucleic acids, useful for preventing, diagnosing and treating, e.g. asthma, inflammation and allergies -

XX Claim 5; Page 39-40; 40pp; English.

XX The invention relates to a novel human Phosphodiesterase type 7B polypeptide and the nucleic acid that encodes it. The protein and nucleic acid may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate phosphodiesterase 7B (P7B) expression. For example, the protein and nucleic acid may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P7B by expressing inactive proteins or to supplement the patients own production of P7B. The nucleic acids may be used to produce P7B

CC polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The nucleic acid and its complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The P7B polypeptides may also be used as antigens in the production of antibodies against P7B and in assays to identify modulators of its expression and activity. The anti-P7B antibodies and antagonists may also be used to down regulate expression and activity. The anti-P7B antibodies may also be used as diagnostic agents for detecting the presence of P7B in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). Disorders that may be prevented, diagnosed and/or treated by the above methods include, for example cardiovascular disease, asthma, allergy, inflammation, and immune-related disorders. The present sequence encodes a human phosphodiesterase 7B.

XX Sequence 1175 BP; 345 A; 281 C; 275 G; 270 T; 4 other;

Query Match 79.5%; Score 1075; DB 22; Length 1175;

Best Local Similarity 97.9%; Pred. No. 0; Mismatches 19; Indels 3; Gaps 3;

Matches 1117; Conservative 2; Mismatches 19; Indels 3; Gaps 3;

QY 154 GCGCTACTTAACAGTACACATACCTCAGGGAGATTGGACCAAGAAAAGGTAAAGA 213  
DB 30 GCGCTACTTAACAGTACACATACCTCAGGGAGATTGGACCAAGAAAAGGTAAAGA 89  
QY 214 CTATTAAAGCTTTCAAGATACCTTCATGATCAAGAGCTGCTGTTGGAATTATACCA 273  
DB 90 CTATTAAAGCTTTCAAGATACCTTCATGATCAAGAGCTGCTGTTGGAATTATACCA 149  
QY 274 GCGCCCTGACACCTGCTGATGAAGAGTACCTTGGACCAAGAGCATATGCTTCCAAA 333  
DB 150 GCGCCCTGACACCTGCTGATGAAGAGTACCTTGGACCAAGAGCATATGCTTCCAAA 209  
QY 334 GTGGGAATGTGGATTTTGAATTTCTTTGTTGATGCTGTCGAATGAAGAGCTG 393  
DB 210 GTGGGAATGTGGATTTTGAATTTCTTTGTTGATGCTGTCGAATGAAGAGCTG 269  
QY 394 GTAAACAGTGTGGACACCTCTTCAATACCAAGAGCTGATCATTGCAATTAAGTAA 453  
DB 270 GTAAACAGTGTGGACACCTCTTCAATACCAAGAGCTGATCATTGCAATTAAGTAA 329  
QY 454 ATGTGACCTTACACCGATTTTATGATGCTTCAAGAAAGATTACACAGCCAAACCCG 513  
DB 330 ATGTGACCTTACACCGATTTTATGATGCTTCAAGAAAGATTACACAGCCAAACCCG 389  
QY 514 TATCACAATGCTGTTACAGGAGCCGACGTACCCAGGCCATGCTGTTACCTGAAGA 573  
DB 390 TATCACAATGCTGTTACAGGAGCCGACGTACCCAGGCCATGCTGTTACCTGAAGA 449  
QY 574 CCAAGAGCTTGGACACCTTCTCAGCCCTGTGACATGCTTGGAGTGTGCTGCACACA 633  
DB 450 CCAAGAGCTTGGACACCTTCTCAGCCCTGTGACATGCTTGGAGTGTGCTGCACACA 509  
QY 634 GCACAGATGTGACACACCCAGGGGTGAACACCAATTTTGTAAACATTAACACCAT 693  
DB 510 GCACAGATGTGACACACCCAGGGGTGAACACCAATTTTGTAAACATTAACACCAT 569  
QY 694 CTGCAAAACCTATATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753  
DB 570 CTGCAAAACCTATATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 629  
QY 754 GGCATGCTTGAGAGATCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813  
DB 630 GGCATGCTTGAGAGATCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689  
QY 814 GAACAGCAGCTGGGCTCTTGTATCTTGGCAACAGACATCAACAGGCAAGATATTTTG 873  
DB 690 GAACAGCAGCTGGGCTCTTGTATCTTGGCAACAGACATCAACAGGCAAGATATTTTG 749  
QY 874 ACCAGATTGAAGGCTCACTCCACATTAAGAGCTGAAGTGAAGTGAAGTGAAGTGAAG 933  
DB 750 ACCAGATTGAAGGCTCACTCCACATTAAGAGCTGAAGTGAAGTGAAGTGAAGTGAAG 809



QY 934 CACTTATGCTTCAGATGCGCTTGAAGTGTGCTGACATTTGCATTCCTTTAGAAATCTGG 993  
 DB 810 CACTTATGCTTCAGATGCGCTTGAAGTGTGCTGACATTTGCATTCCTTTAGAAATCTGG 869  
 QY 994 GAGATGAGCAAGCAGTGAAGTGAAGGCTCTGTGAAGATTTACAGGCAAGTGAACCT 1053  
 DB 870 GAGATGAGCAAGCAGTGAAGTGAAGGCTCTGTGAAGATTTACAGGCAAGTGAACCT 929  
 QY 1054 GAGCAAGATTTGAACCTGGAATTCAGTCTCTTTTATCAACAGAAAGATTCATCCCT 1113  
 DB 930 GAGCAAGATTTGAACCTGGAATTCAGTCTCTTTTATCAACAGAAAGATTCATCCCT 989  
 QY 1114 ACTATACAAATTTGTTTATGATGATACATCGTGAAGCGCTCTTCCGGGAATGGGCCAT 1173  
 DB 990 ACTATACAAATTTGTTTATGATGATACATCGTGAAGCGCTCTTCCGGGAATGGGCCAT 1049  
 QY 1174 TTTACAGGGTAAACAGACACCTGTGCGAGAAACATGCTGGGCGACC-TGCGACACAGAGGC 1232  
 DB 1050 TTTACAGGGTAAACAGACACCTGTGCGAGAAACATGCTGGGCGACC-TGCGACACAGAGGC 1108  
 QY 1233 CCAAGTGAAGACCTGTTGCTCCAGCAGACAGAAAGAGGCGAGCATGGCAGCGGCC 1292  
 DB 1109 CCAAGTGAAGACCTGTTGCTCCAGCAGACAGAAAGAGGCGAGCATGGCAGCGGCC 1167  
 QY 1293 T 1293  
 DB 1168 T 1168

RESULT 8  
 ID AAA46552  
 ID AAA46552 standard; CDNA: 2992 BP.

AC AAA46552;

DT 25-SEP-2000 (first entry)

DE CDNA of a human phosphodiesterase gene.

XX Phosphodiesterase; PDE-XIV; murine; enzyme; ss.

OS Homo sapiens.

PN EP1018559-A1.

PD 12-JUL-2000.

PF 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PF12 ) PRIZER LTD.

PA (PF12 ) PRIZER INC.

PI FidoM; M;

DR WPI: 2000-433274/38.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,

XX useful for preventing diagnosing and treating diseases associated with

XX inappropriate PDE-XIV expression and/or activity -

XX Example: Page 49-51; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV cDNA. The

CC phosphodiesterase polynucleotide and polypeptide may be used in the

CC prevention, treatment and diagnosis of diseases associated with

CC inappropriate PDE-XIV expression. For example, the polynucleotide

CC be administered to treat diseases by rectifying mutations or deletions

CC in a patient's genome that affect the activity of PDE-XIV. They may

CC polypeptides and their role in metabolism. The PDE-XIV polypeptides  
 CC may be used as antigens in the production of antibodies against PDE-XIV  
 CC and in assays to identify modulators (agonists and antagonists) of  
 CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and  
 CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression  
 CC and activity (i.e. the PDE-XIV gene and/or expression product may be  
 CC used in the preparation of a composition for the treatment of a disorder  
 CC associated with inappropriate PDE-XIV expression and/or activity and to  
 CC screen for agents that can modulate PDE-XIV expression and or activity.  
 CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for  
 CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by  
 CC enzyme linked immunosorbent assay (ELISA)).  
 XX

SO Sequence 2992 BP: 890 A: 612 C: 609 G: 881 T: 0 other:

Query Match 59.4%; Score 803.2; DB 21; Length 2992;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-241;  
 Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCTGTGTTTATGTTGAGAGGTGGGCGAAATCTGTTGAGAACCCGATCAGAT 60  
 DB 298 ATGCTGTGTTTATGTTGAGAGGTGGGCGAAATCTGTTGAGAACCCGATCAGAT 357  
 QY 61 GCCAATGCTGTTGATGCTGGAGATATACGACTAAGGGCTCAGACGGGGTGTGCT 120  
 DB 358 GCCAATGCTGTTGATGCTGGAGATATACGACTAAGGGCTCAGACGGGGTGTGCT 417  
 QY 121 GAGCGCGTGGCTCTACCCATTCATTCGCTTACCTTACAGATACATCTCA 180  
 DB 418 GAGCGCGTGGCTCTACCCATTCATTCGCTTACCTTACAGATACATCTCA 477  
 QY 181 GGGGAGTTGGGACCAAGAAAGTGAAGAACTATTAAGCTTCAAGATCTTCAT 240  
 DB 478 GGGGAGTTGGGACCAAGAAAGTGAAGAACTATTAAGCTTCAAGATCTTCAT 537  
 QY 241 GCATCAAGGCTGCTCTGTTGATATACCAAGCCCTCTGACCTGCTGATGAAGAC 300  
 DB 538 GCATCAAGGCTGCTCTGTTGATATACCAAGCCCTCTGACCTGCTGATGAAGAC 597  
 QY 301 TACCTTGGACAAAGCAAGGATATGCTCTCAAGTGGGATGGGATTTTACATTTTC 360  
 DB 598 TACCTTGGACAAAGCAAGGATATGCTCTCAAGTGGGATGGGATTTTACATTTTC 657  
 QY 361 TTTGTTGATCGCTTACCAATGGAAGCCCTGTATACCTGTGGCACCCTTCAT 420  
 DB 658 TTTGTTGATCGCTTACCAATGGAAGCCCTGTATACCTGTGGCACCCTTCAT 717  
 QY 421 ACCCATGACATTCATTCACATTTCAAGTTAGTGTGACCTTACACGATTTTATGTC 480  
 DB 718 ACCCATGACATTCATTCACATTTCAAGTTAGTGTGACCTTACACGATTTTATGTC 777  
 QY 481 ATGTTTCAAGAAAGATTACCAAGCCCAAAACCGGTATACATGCTGTTCACGACCGAC 540  
 DB 778 ATGTTTCAAGAAAGATTACCAAGCCCAAAACCGGTATACATGCTGTTCACGACCGAC 837  
 QY 541 GTACCCAGGCGCATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 600  
 DB 838 GTACCCAGGCGCATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 897  
 QY 601 CTGCAATCATCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 DB 898 CTGCAATCATCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957  
 QY 661 AACCAAGCCATTTTATATAAACTAACCAAGCCATTTTATATAAACTAACCAAGCC 720  
 DB 958 AACCAAGCCATTTTATATAAACTAACCAAGCCATTTTATATAAACTAACCAAGCC 1017  
 QY 721 GTGCTGAGAAATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 DB 1018 GTGCTGAGAAATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077  
 QY 781 GCTCATTTGCCAAGAAATGACACAG 808  
 |||||||||||||||||||||

Db 1078 GCTCATTTGCCAAGAAAGATGACGTAAAG 1105

## RESULT 9

ID AAA46650 standard; DNA: 807 BP.

AC AAA46650:

25-SEP-2000 (first entry)

DE DNA encoding a human phosphodiesterase enzyme.

KW Phosphodiesterase; PDE-XIV; human; enzyme; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS

1..807

FT /product= "phosphodiesterase"

FT /note= "the codons encoding amino acids 269-288 are not given"

PN EP1018559-A1.

PD 12-JUL-2000.

PP 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PFIZ ) PFIZER LTD.

PA (PFIZ ) PFIZER INC.

PI Fidoack M:

DR WPI: 2000-433274/38.

DR P-FSDB; NAI93568.

PS Claim 4; Page 44; 104pp; English.

The present sequence encodes a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA)).

Sequence 807 BP; 224 A; 197 C; 180 G; 206 T; 0 other;

Query Match 59.3%; Score 803; DB 21; Length 807;

Best Local Similarity 100.0%; Pred. No. 7.4e-242; Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTTAAATGTTGAGAGGTGTGGGAAATCTTGTGAGAACCCGATCAGANT 60  
Db 1 ATGCTGTTTAAATGTTGAGAGGTGTGGGAAATCTTGTGAGAACCCGATCAGANT 60  
QY 61 GCCAAATGTGTTGATGCTGGGAGATATACGACTAAGGGGTGACAGCGGGGTGCTGCT 120  
Db 61 GCCAAATGTGTTGATGCTGGGAGATATACGACTAAGGGGTGACAGCGGGGTGCTGCT 120  
QY 121 GAACGCCGTGGCTCTACCATTCATTTGACCTTCCCTACTTAACAGTCAACATACCA 180  
Db 121 GAACGCCGTGGCTCTACCATTCATTTGACCTTCCCTACTTAACAGTCAACATACCA 180  
QY 181 GGGAGATTTGGACACCAAGAAAAGTGAAGAAAGCTATTAAGCTTTCAAAGATCTTCAT 240  
Db 181 GGGAGATTTGGACACCAAGAAAAGTGAAGAAAGCTATTAAGCTTTCAAAGATCTTCAT 240  
QY 241 GCATCAAGGCTGCTTGTGGAATTTATACCAAGCCCTCTGACCTGCTGATGAAGAC 300  
Db 241 GCATCAAGGCTGCTTGTGGAATTTATACCAAGCCCTCTGACCTGCTGATGAAGAC 300  
QY 301 TACCTTGAGACAGCAAGCATATGCTCTCCAAAGTGGAGATTTGGACATTTTC 360  
Db 301 TACCTTGAGACAGCAAGCATATGCTCTCCAAAGTGGAGATTTGGACATTTTC 360  
QY 361 TTGTTTATGCTTGACAAATGGAACAGCCTGTGTACACTGTGTGTCACCTCTTCAAT 420  
Db 361 TTGTTTATGCTTGACAAATGGAACAGCCTGTGTACACTGTGTGTCACCTCTTCAAT 420  
QY 421 ACCCATGACATTCACATTCATTCAGTTAGATATGATGATGATGATGATGATGATG 480  
Db 421 ACCCATGACATTCACATTCATTCAGTTAGATATGATGATGATGATGATGATGATG 480  
QY 481 ATGTTCAAGAAAGTATCCACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 540  
Db 481 ATGTTCAAGAAAGTATCCACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 540  
QY 541 GTGACCCAGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 541 GTGACCCAGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
QY 601 CTGGACATCATGCTTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 601 CTGGACATCATGCTTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
QY 661 AACGAGCCATTTTGTATTAATAAATAACCAACCATCTTGCAAACTATATCAGATATG 720  
Db 661 AACGAGCCATTTTGTATTAATAAATAACCAACCATCTTGCAAACTATATCAGATATG 720  
QY 721 GTGCTGGAGATATCATCTGCGATCTACAAATTTGGATGCTTGCAGAAATCAAGCTT 780  
Db 721 GTGCTGGAGATATCATCTGCGATCTACAAATTTGGATGCTTGCAGAAATCAAGCTT 780  
QY 781 GCTCATTTGCCAAGAAAGATGAC 803  
Db 781 GCTCATTTGCCAAGAAAGATGAC 803

RESULT 10  
AACB7949  
ID AACB7949 standard; cDNA: 3336 BP.  
AC AACB7949:  
DT 06-MAR-2001 (first entry)  
XX Human short phosphodiesterase encoding cDNA SEQ ID NO:4.  
DE  
XX Human; long phosphodiesterase; short phosphodiesterase; diagnosis;  
KW cyclic nucleotide phosphodiesterase; noctropic; cardiant; hypotensive;  
KW nephropathy; antidepressant; antiinflammatory; immunosuppressive;  
KW antifertility; antistatic; gene therapy; dementia;  
KW amnesia; congestive heart failure; thrombosis; pulmonary hypertension;  
KW glomerulonephritis; bipolar depression; bronchial asthma; salt retention;

KM atopic disease; autoimmune encephalomyelitis; organ transplantation;  
 KM nephrotic syndrome; erectile dysfunction; ss.  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 223..1185  
 FT /tag= a  
 FT /product= "short phosphodiesterase"  
 FT /note= "cyclic nucleotide phosphodiesterase"  
 XX  
 XX US6146876-A.  
 XX  
 PD 14-NOV-2000.  
 XX  
 PF 11-JUN-1999; 99US-0330970.  
 XX  
 PR 26-MAR-1999; 99US-0277423.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 PI Kapeller-Libermann R, White D, Robison KE;  
 DR WPI: 2001-023577/03.  
 DR P-PSDB; AAB36504.  
 XX  
 XX  
 PT Polynucleotide encoding novel cyclic nucleotide phosphodiesterase  
 PT useful for treating disorders related with to protein e.g. dementia,  
 PT hypertension, glomerulonephritis, and organ transplantation  
 XX  
 PS Claim 1; Fig 6; 42pp; English.  
 XX  
 CC The present sequence encodes the human short phosphodiesterase which  
 CC is a cyclic nucleotide phosphodiesterase (1). (1) can have neurotropic,  
 CC cardiant, hypotensive, nephrotropic, antidepressant, antiinflammatory,  
 CC immunosuppressive, antifertility, antiasthmatic and vasotrophic  
 CC activities, and can be used in gene therapy. (1) can be used for  
 CC treating various disorders associated or mediated by (1), such as  
 CC dementia, amnesia, congestive heart failure, thrombosis, pulmonary  
 CC hypertension, glomerulonephritis, bipolar depression, bronchial asthma,  
 CC atopic diseases, autoimmune encephalomyelitis, organ transplantation,  
 CC salt retention in nephrotic syndrome and erectile dysfunction.  
 XX  
 SQ Sequence 3336 BP; 1011 A; 682 C; 695 G; 947 T; 1 other:  
 \* Query Match 53.5%; Score 723.8; DB 22; Length 3336;  
 Best Local Similarity 99.0%; Pred. No. 1.5e-216;  
 Matches 728; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 434 TTCACCATTTCAAGTATAGATATGTGACCTTACACCGATTTTATGATCGTTCAAGAAG 493  
 |||||||  
 DB 812 TTCACCATTTCAAGTATAGATATGTGACCTTACACCGATTTTATGATCGTTCAAGAAG 871  
 OY 494 ATTACCAAGCCAAACCCGATACAAATGCTTTCACGAGCCGACGATCCAGGCCA 553  
 |||||||  
 DB 872 ATTACCAAGCCAAACCCGATACAAATGCTTTCACGAGCCGACGATCCAGGCCA 931  
 OY 554 TGCACCTGCTACCTGAAAAGACCAAGCTTCCACGCTTCTCAGACCTCTGGACATATGC 613  
 |||||||  
 DB 932 TGCACCTGCTACCTGAAAAGACCAAGCTTCCACGCTTCTCAGACCTCTGGACATATGC 991  
 OY 614 TTGACCTGCTGCTGCGAGCAGCACAGATGTGACCAACCCAGGGGTGAACACCAATTTT 673  
 |||||||  
 DB 992 TTGACCTGCTGCTGCGAGCAGCACAGATGTGACCAACCCAGGGGTGAACACCAATTTT 1051  
 OY 674 TGATAAAAAATCAACACCATCTTGCACCAACCTATATGAGATATGCTGTGAGAAATC 733  
 |||||||  
 DB 1052 TGATAAAAAATCAACACCATCTTGCACCAACCTATATGAGATATGCTGTGAGAAATC 1111  
 OY 734 ATCACTGGCGATCTACAAATTTGGCATGCTTGAGAAATCAAGGCTTTCTCATTTGCCA 793  
 |||||||  
 DB 1112 ATCACTGGCGATCTACAAATTTGGCATGCTTGAGAAATCAAGGCTTTCTCATTTGCCA 1171  
 OY 794 AGGAATGACACAGG 808  
 |||||||  
 DB 1172 AGGAATGACGTTAAG 1186  
 RESULT 11  
 AAQ14629  
 ID AAQ14629 standard; DNA; 3987 BP.  
 AC AAQ14629;  
 XX  
 XX 30-JAN-1992 (first entry)  
 DT  
 XX  
 DE Human Glioblastoma cell CDNA.  
 XX  
 KW phosphodiesterase; PDE; PTM22; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 3..1498  
 FT /tag= a  
 XX  
 XX W09116457-A.  
 XX  
 PD 31-OCT-1991.  
 XX  
 PF 19-APR-1991; 91WO-US02714.  
 XX  
 PR 20-APR-1990; 90US-0511715.  
 XX  
 PA (COLD-) COLD SPRING HARBOR.  
 XX  
 PI Wiggler MH, Colicelli JJ;  
 XX  
 DR WPI: 1991-339841/46.  
 XX  
 PT Complementary screening for genes and prods. - e.g. RAS protein  
 PT and cAMP, that modify, complement or suppress genetic defect and  
 PT correct associated phenotypic alteration  
 XX  
 PS Example 1C; Page 84; 169pp; English.  
 XX  
 CC In the specification this sequence is given the SEQ ID NO.19 which  
 CC is described as the cDNA insert of plasmid PTM22. Plasmid PTM22 in  
 CC E.coli (ATCC 86601) is described as containing a human glioblastoma  
 CC cell cDNA insert encoding a PDE of unclassifiable family  
 CC designation. N.B. many of the references in the text of the  
 CC specification to particular sequences are incorrect, therefore

CC caution is advised in accepting that this sequence is indeed pTM22 i  
 XX Sequence 3987 BP; 1137 A; 802 C; 818 G; 1222 T; 8 other;  
 S0

Query Match 37.0%; Score 500.6; DB 12; Length 3987;  
 Best Local Similarity 62.9%; Pred. No. 2.9e-146;  
 Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

18 TGAAGAGTGGCGAAATCTGTTGGAACCCGATCCAGAAATGCCAAATGTTGGAT 77  
 185 TCACAGGCGTGGACCTATTTCTATGACAGTCTGATCAGACGCTATATACATTCGTAT 244  
 78 GCTGGAGATATACGATTAAGGGGTGACAGCGGGGTTGCTGGAAAGCGCGGCGCTCA 137  
 245 GCTAGAGATGTACGTGAAGAGCCGAGAGGATTTGAAATCAGAAAGAGAGGTTCTCA 304  
 138 CCCATCATTTGACTTCGCGCTTACATTAAGTACATCTACGAGGAGATTTGGACCA 197  
 305 CCCATATTTGATTTTGTCTATTTCCACTCTCAATCTGAATTTGAAGTGTCTGTCTGC 364  
 198 GAAAAAGGTGAAAAAGACTATTAAAGCTTTCAGAGATCTTCATGCATCAAGCGCTCTGC 257  
 365 AAGGAATATCAGAAAGGCTACTAAGATTTCAGAGATATCTAGATCTTCACGCTTTTTCG 424  
 258 TGAATATATACCAAGCCCTCTGCACCTGTGATGAAGACTACCTTGGACAAGCAAG 317  
 425 TGGTACGTGGGTTTCAAAATTCCTTAACATTTTGAATGATGATTAATGAAGCAAGCCAA 484  
 318 GCATATGCTCTCCAAAGTGGGAATGTGGATTTTGAATTTCTGTTTGAATCGCTTGC 377  
 485 GTGATGCTGTGAAAAAGTTGGAATTTGATTTGATTTCTTCAATTTGATGAGACTTAAC 544  
 378 AATGGAACAGCCTGTGTAACGTTGTGCGCACCTCTCAATTAACAGCTGAGCTATCA 437  
 545 AATGGAATATGCTAGTACTTAAGCTTAACCTTTCAATTTATTAGCTCAATGATTAATGA 604  
 438 CCATTTGAGTTGATATGTTGACCTTACACGATTTTATGATGATGATGATGATGATGAT 497  
 605 GTACTTCCATTTAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664  
 498 CCAGAGCCAAACCCGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 557  
 665 CCACAGTCAATATCTTACATTAAGAGAGTCCAGGCTGCGATGATGATGATGATGATGAT 724  
 558 CTGCTACCTGAAGAGCCAAAGCTTGCACGCTTCTACGCTCTGAGATCATGCTTGG 617  
 725 CTGTTACTTAAAGAACCTTAAGCTTACGATTTCTGTAATCTCTGGATATCTTGTAG 784  
 618 ACTGCTGCTGACAGCAGCAGCAGATGTGACCAAGGAGGAGTGAACCAAGCTTTTGTAT 677  
 785 CTTAATGACAGCTGCCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 844  
 678 AAAAACTAACCCATCTTCAAACTATATATGATGATGATGATGATGATGATGATGATGAT 737  
 845 TAAAACTAACCATTTACTTGGCACTTATATCAAGAAATACCTGATCTGAAATACACCA 904  
 738 CTGGGATCTACAATTTGCTGAGATATCAAGCTTCTTGGCTGATTTGCCAAAGCA 797  
 905 CTGAGATCTGAGATGAGCTTTATGAGAGATAGGCTTATCTCATCATCTGCCATTGA 964  
 798 AATGACAGGATATTTAAGAGAGCGGCTCTGATCTGATCTGATCTGATCTGATCTGATCT 857  
 965 AAGGAGCACAATATGAGACACAGATAGTGTCTGATCTGATCTGATCTGATCTGATCTG 1024  
 858 GCAAGATGATTTTGAACGATTTGAAGCTCACTCCCAATTAAGCTTAAAGCTTGAAGCT 917  
 1025 CCAAGATGATCTGCTTGTGTTGAGTCCATTTGGATTAAGGATGATTTGCTTGA 1084  
 918 GGATGACAGCAGGACCTTATGCTTGAATGCTGCTGAAAGTGTGCTGATTTGGCA 977  
 1085 AGACACGACAGACAGATTTGTTTACAGATGCTTTGAAATGCTGCTGATTTGTTGA 1144  
 978 TCCTTTGATGATCTGGAGATGAGCAAGAGTGGAGTGAAGGCTCTGTAAGATTTCTA 1037

1145 CCCATGTCGAGACGTGGGAATTAAGCAGACGAGTGAATAAAGTAAACGAGGAAATCTT 1204  
 1038 CAGCAGAGGTGAACCTTGAACAGAAATTTGAACCTGGAATTCAGCTCTCTTTGTAATCA 1097  
 1205 CCATCAAGGAGATATGAAAAAATATCATATTTGGGTGTGATGCTACATTCGTCA 1264  
 1098 GAAAGATTCATCCCTAGTATCAAAATTTGTTTCAATGAGCTACATTCGAGAGCCGCTCT 1157  
 1265 CACTGATATGATGCCAATCATCCAGATTTGTTTATGATTAACCTAGTGGAGCCTTAT 1324  
 1158 CCGGAAATGGGCGCATTTACGAGGTGAACAGCCCTGTGCGAAGAAACATGCTGGCCAC 1217  
 1325 TACAGATGGCGCAGGTTTC---CATATCAAGGCTATCCACAGACATGCTGAGACGT 1381  
 1218 CGACACAAACAGCCGACAGTGAAGAGCTGTGCGCCAGGACGACAGCAAGAGGCA 1276  
 1382 GGGGCTGAATTAAGCCAGCTGGAAGGAGCTGCAGAGAGACAGTCGACAGTGAAGCA 1440

## RESULT 12

AAT34376  
 ID AAT34376 standard; cDNA; 3987 BP.

XX AAT34376;

XX 09-OCT-1996 (first entry)

XX Plasmid pTM22 (ATCC 68601) insert.

XX Human; glioblastoma cell; heat shock sensitivity; phosphodiesterase;  
 XX deficient yeast strain 10DAB; pTM22; rat pD phosphodiesterase; pde1-;  
 XX bovine Ca2+/calmodulin dependent CAMP phosphodiesterase; heart; plasmid;  
 XX RAS2(val19); pde2; pTM2; PRATPD; pUC9; rolipram sensitive; ss.

XX Homo sapiens.

XX key Location/Qualifiers

XX CDS 3..1499 /tag= a

XX FT /product= CAMP phosphodiesterase

XX US5527896-A.

XX 18-JUN-1996.

XX 20-APR-1990; 90US-0511715.

XX 19-APR-1991; 91US-0688352.

XX 20-APR-1990; 90US-0511715.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Colicelli JJ, Wigler MH;

XX WPI; 1996-299902/30.

XX P-PSDB; AAM00094.

XX Claim 4; Column 67-70; 101pp; English.

XX The sequences given in AAT34374-76 represent plasmid fragments which  
 XX contain human glioblastoma cell cDNA inserts which are capable of  
 XX correcting the heat shock sensitivity of the phosphodiesterase  
 XX deficient yeast strain 10DAB. Several cDNA's were isolated and  
 XX sequenced. pTM22 encodes a novel human gene. From computer analysis,  
 XX pTM22 putatively encodes a protein homologous to various CAMP  
 XX phosphodiesterases, such as the bovine Ca2+/calmodulin dependent CAMP  
 XX phosphodiesterase and the rat pD phosphodiesterase. Sequences related  
 XX to pTM22 were found to be expressed in human heart. Plasmid pTM22 was  
 XX unable to correct the heat shock sensitivity of RAS2(val19) Yeast

CC strains. It thus appears that the pde1- and pde2- yeast strain 10DAB  
 CC is more sensitive to phenotypic reversion by mammalian cAMP.  
 CC phosphodiesterase clones than is the RAS2(vall19) yeast strain. The  
 CC inserts in the plasmids pTM3 and pTM72 were also characterised. These  
 CC two different cAMP phosphodiesterase cDNA's were found to be closely  
 CC related to, but distinct from, the pRATPD insert and the pJC99 insert.  
 CC Biochemical analysis of cell lysates has established that the cDNA's of  
 CC pTM3 and pTM72, pJC44x and pRATPD encode rolipram sensitive cAMP  
 CC phosphodiesterases.  
 XX  
 SQ Sequence 3987 BP; 1137 A; 803 C; 817 G; 1222 T; 8 other:  
 Query Match 37.0%; Score 500.6; DB 17; Length 3987;  
 Best Local Similarity 62.9%; Pred. No. 2.9e-146;  
 Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;  
 QY 18 TGAAGAGTGGCGCAATCTGTTTGAAGACCCGATCAGAAATGTCAT 77  
 DB 185 TCAGAGGGGTGAGACTATTTCTATGACAGTTCGATCAGACTGATTAATCGTAT 244  
 QY 78 GCTGGAGATATACAGACTATAGGGGTCAGAGGGGGTGTGCTGTAAGCCGTCCTA 137  
 DB 245 GCTAGAGATATGAGTGTAGAGAGCCGAGAGATTTGAATCAGAAAGAGGTTCTCA 304  
 QY 138 CCATTCATGACTTCGCTTACTTAACAGTACACATATCTCAGGGGAGATTGGACCAA 197  
 DB 305 CCCATATATGATTTTGTATTTTCCACTCCATATCTGAATGAAAGTCTGTCTGCTGC 364  
 QY 198 GAAAAAGGTGAAAGACTATTAAAGCTTTCAAGATACTTCCATGATCAGAGGCTTCG 257  
 DB 365 AAGGAATATCAGAAAGGCTACTAAGTTCCAGCATATCTTGAATCTCACCCTTTTTCG 424  
 QY 258 TGSATTTATACACAAGCCCTCGACCCCTGAGTGAAGAACATCCTTGAAGCAAG 317  
 DB 425 TGATCTCGGCTTCAATTCCTTAACATTTTATGATATATTAATGAAGCAAGCAAG 484  
 QY 318 GCATATGCTCTCCAAAGTGGATGTGGATTTTGACATTTTCTGTTTGAATCCGCTGAC 377  
 DB 485 GTGATGTGGAAAAAGTGGAAATTTGGAATTTGATATCTTCTGATTTGATAGCTAAC 544  
 QY 378 AAATGGAAGACGCTGTGACACTGTGTGTCACCTCTTCAATCCAGTGAATCTTCA 437  
 DB 545 AAATGGAATAGTCTAGTAAGCTTAACCTTCAATTTATTTAGTCTTCAATGATTAATGA 604  
 QY 438 CCATTTCAATTAATAGTGTGACCTTACACCGATTTTATGATAGTGTCAAGAAAGATA 497  
 DB 605 GTACTTCATTTAGATAGTAAAGCTTGTAGATTTTATTAATTAAGAAAGATTA 664  
 QY 498 CCACAGCCAAACCCGATACAAATGCTTACAGCAGCAGCAGCCAGCCAGCCATGCA 557  
 DB 665 CCACAGTCAAAATCTTACATTAAGCAGTCCAGCTCGGATGTTACTCAGGCCATGCA 724  
 QY 558 CTGCTACCTGGAAGAGCCAAAGCTTCCAGCTTCCCTCAAGCCCTGACATCATGCTTGG 617  
 DB 725 CTGTACTTAAGAACCTTAAGCTTCCCAATTCGTAACCTCTTGGGATATCTTGGCTAG 784  
 QY 618 ACTGCTGCTCAGCAGACAGATGTGACACCCAGGGGTGAACAGCCATTTTAT 677  
 DB 785 CTTAATTCAGCTCCCATCTAGATGATCTGATATCCAGGTATTAATCAACCTTTCCTTAT 844  
 QY 678 AAAAATCAACCACTTGTGAACCTTATCAGAAATGCTGTGAGGAATCATCA 737  
 DB 845 TAAATCACTATTAATCTTGGCACTTTTACAGAAATCTCAGTACTGGAAATACCA 904  
 QY 738 CTGGGATCTCAATTTGGCATGCTTCCGAAATCAAGGCTTGTGCTCAATTTGCCAAGAG 797  
 DB 905 CTGAGATCTCAGTGGGCTTATGAGAGAAATCAGGCTTATTCACATCTGCCATTTGA 964  
 QY 798 AATGACACAGATATTTGAACAGCAGCTGGCTCTGTGATCTTGGCAACAGATCAACAG 857  
 DB 965 AAGCAGGCAAAATTTGGAGACAGATAGGTCTCTGATTAAGCAGACAGATCAGTCG 1024  
 QY 858 GCAGATGATTTTGTGACCAAGATTAAGGCTCACCCTCCACAATAAAGCTTAAGACTGA 917

DB 1025 CCAGATAGATATCTGCTTTGTTAGTCCCATTTGGATAGAGGTGATTTATGCTTGA 1084  
 QY 918 GGATCCACAGCAGCAGCCACTTATATGCTTCAGATCCCTTGAAGTGTGCTGACATTTGCA 977  
 DB 1085 AGACCCAGACACAGCATTTGGTTTACAGATGGCTTGAATGTGCTGATATTTGTAA 1144  
 QY 978 TCCTGTGAATCTGTGGAGATGAGCAGACAGTGAAGTGAAGAGTGTGTAAGAAATCTTA 1037  
 DB 1145 CCATGTGCGAGCTGGGAATTAAGCAGACGTGGAGTGAAGAAATTAAGGAGAAATTTCTT 1204  
 QY 1038 CAGGCAAGTGAATCTGTAACAGAAATTTGAATGAAATTCAGTCTTGTATTAACAA 1097  
 DB 1205 CCATCAAGAGATATAGAAAAAATATCATTTTGGTGTGATCCATTTGGATGTCACA 1264  
 QY 1098 GAAAGATTCATCCCTAGTATTAACAAATTTGTTTCAATGAGCTATCATCTGAGAGCCCTCT 1157  
 DB 1265 CACTGAATCTATTTGCAACATCTCAGATTTGTTTGTACTTAACCTAAGTGAGACCTTTAT 1324  
 QY 1158 CCGGATGGGCCCCATTTACAGGGTAAACAGCACCCCTGTGCGAGAACATGTTGGCCACT 1217  
 DB 1325 TACAGATATGGCCAGGCTTTTC--CAATACAAAGCTATATCCAGACATATGTTGGACACT 1381  
 QY 1218 CGCACACAAAGGCCAGTGGAGAGGCTGTTGCCAGGACGACAGAACAGGAGCA 1276  
 DB 1382 GGGGCTGAATTAAGCCAGCTGGAAGGAGCTGCAGAGAGAACAGTGCAGCATGAGAGCA 1440  
 RESULT 13  
 AA332240  
 ID AA332240 standard; cDNA; 3987 BP.  
 XX  
 AC AA332240;  
 XX  
 DT 19-JAN-2000 (first entry)  
 XX  
 DE Human glioblastoma cell cAMP phosphodiesterase pTM22 encoding cDNA.  
 XX  
 KW Phosphodiesterase; dunce-like phosphodiesterase; PDE; PD; cAMP;  
 KW RAS-related protein; immunoreactive; detection; genetic defect;  
 KW bronchodilation; increased myocardial contractility;  
 KW anti-inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US5977305-A.  
 XX  
 PD 02-NOV-1999.  
 XX  
 PE 07-JUN-1995; 95US-0474379.  
 XX  
 PR 01-MAR-1994; 94US-0206188.  
 PR 20-APR-1990; 90US-0511715.  
 PR 19-APR-1991; 91US-0688352.  
 XX  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PI Colicelli JJ, Wigler MH;  
 XX  
 DR WPJ; 1999-619709/73.  
 DR P-PSDB; MAY49808.  
 XX  
 PT New isolated RAS-related polypeptides and mammalian cyclic nucleotide  
 PT phosphodiesterases, used for screening for agents which can modify  
 PT complement or suppress genetic defects  
 XX  
 PS Example 1; Column 81-84; 145pp; English.  
 XX  
 CC The present invention describes new isolated RAS-related polypeptides  
 CC and mammalian cyclic nucleotide phosphodiesterases (PDEs). RAS-related  
 CC polypeptides are capable of complementing a defective RAS function in  
 CC yeast. The products can be used for screening for agents which can  
 CC modify, complement or suppress a genetic defect in a biochemical

CC pathway in which cAMP participates, or in a biochemical pathway which  
CC is controlled, directly or indirectly, by a Ras protein and other  
CC proteins affecting cell growth and maintenance. Developing agents that  
CC will selectively act upon PDEs is directed toward reproducing the  
CC desirable effects of cyclic nucleotides, e.g. bronchodilation,  
CC increased myocardial contractility, anti-inflammation, yet without  
CC causing the undesirable effects, e.g. increased heart rate or enhanced  
CC lipolysis. The products can also be used for therapeutic, diagnostic  
CC and prognostic uses. AA32229 to AA32285, and AA49803 to AA49830,  
CC represent sequences used in the exemplification of the present  
CC invention.

XX Sequence 3987 BP: 1137 A; 803 C; 817 G; 1222 T; 8 other:

Query Match 37.0%; Score 500.6; DB 20; Length 3987;  
Best Local Similarity 62.98; Pred. No. 2.9e-146;  
Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

QY 18 TGAAGAGTGTGCGAAATCTTGTGTGAGAACCCGATCAGAAATGCTTTGAT 77  
DB 185 TCAGAGGCGTGGAGCTATTTCTTATGACAGTTCGATCAGCTCATTAATACATCTAT 244  
QY 78 GCTGGAGATATACGACTAAGGGGTACAGCGGGGTCTGCTGTAACGCCGTGCTCTTA 137  
DB 245 GCTAGAGAGTGTACGTGTAAGAGCGGAGGAGATTGGAATCAAGAAAGAGGTTCTCA 304  
QY 138 CCCATCATGTGACTTCCGCTACTTAACAGTACAACTACTCAGGGGAGATTGGACCAA 197  
DB 305 CCCATCATGTGATTTCGATTTTCCATCTCAATCTGAATTAAGTGTCTGTCTGTC 364  
QY 198 GAAAAAGTGAAGAACATTAAGCTTCAAGTACTTCCATCATCAAGGCTGCTTG 257  
DB 365 AAGGATATCAAGAGCTACTAATGTTCCAGCAGATCTTATGATCTTCAGCTTTTTCG 424  
QY 258 TGGAAATATACCAAGGCCCTCTGCACCTGTGATGAGACACTTCTGGACAAAG 317  
DB 425 TGGTACTGGGTTCAAAATCCCTTAACATTTTATGATGATATATATGACAGGCNA 484  
QY 318 GCATATGCTCTCCAAAGTGGGAGATGGGATTTTGACATTTTCTGTTGATCGCTGAC 377  
DB 485 GTGTATGCTGGAAGAAAGTGAATTTGAAATTTGATATCTTTTATTTGATACATAAC 544  
QY 378 AAATGAAACAGCCTGATACACTGTTTGCACCTCTTCAATCCCATGAGACTATCA 437  
DB 545 AAATGAAATAGCTAGTAAGCTTAACCTTCAATTTATTTAGCTTCATGATTAATGA 604  
QY 438 CCATTTCAAGTATGATATGCTGACCTTACACCGATTTTATGATGCTCAAGAGATTA 497  
DB 605 GTACTTCCATTTAGATATGATGAACTTCGTAGATTTTATGATTAAGTAAGATTA 664  
QY 498 CCACAGCCAAAACCCGTTACAAATGCTTACAGCAGCCGATCCAGCCGACATGCA 557  
DB 665 CCACAGTCAAAATCCCTTACCAATAGCAGTCCAGCTCGGATTTTACTCAGGCCATGCA 724  
QY 558 CTGCTACTGGAAGAGCCAAAGCTTCCAGCTTCTCAGCGCTCTGACATCATGCTTG 617  
DB 725 CTGTTACTTAAAGAACTTAAGCTTCAATCTGTAATCTCTGGGATCTTGCTGAG 784  
QY 618 ACTGCTGCTGACAGACAGCAGATGTGACCCAGCGGGGTGAACGACCATTTTGTAT 677  
DB 785 CTTAATTTGAGTGCACATGATCTGATATCCAGAGTGTATATTAACCTTCTAT 844  
QY 678 AAAAATCAACACCATCTTTCGAAACCTTATACAGATATGTCTGCTGAGATCTTCA 737  
DB 845 TAAACTATACCATTTACTTGGCAATTTATACAGAAATCTCACTACTGGAATAACCA 904  
QY 738 CTGGGAGATTAATTTGATGCTTCCGAAATCAAGGCTTCTGCTATTTGCCAAAGGA 797  
DB 905 CTGGAGATGTGAGTGCGCTTATGAGAAATCAAGGCTTATTCACATCTGCCATTTAGA 964  
QY 798 AATGACACAGATATTTGAACAGCAGCTGGCTCTTATCTTGGCAACAGATCAACAG 857  
DB 965 AAGCAGGCAACAATGAGAGACACAGATAGTGCTGTCTACTTACCCACAGACATCACTG 1024

QY 858 GCAGATGATTTTTTGGACCAAGATTTGAAGGCTCACCTCCACAAATTAAGACTGGA 917  
DB 1025 CCAGATGATGATCTGCTTTGTTAGCTCCCAATTTGATGAGGATGATTTATGCTTGA 1084  
QY 918 GGATGACAGGACGAGCATTTATGCTTCAGATCGCCTTGAAGTGTGCTGATTTGCA 977  
DB 1085 AGACCCAGACACAGACATTTGTTGTTTACAGATGGCTTTGAAATGCTGATATTTGTA 1144  
QY 978 TCCCTGTAGATATGAGAGATGAGCAAGCAGTGTGAGTGAAGGCTGTGCAATTTCTA 1037  
DB 1145 CCCATGTGCGACGTGGGAATTTAAGCAAGCAGTGTGAGTGAAGGCTGTGCAATTTCTT 1204  
QY 1038 CAGGCAAGGTGACTTTAACAAGAAATTTGACTGGAATTCAGTCTTTGTAATCA 1097  
DB 1205 CCATCAAGAGATATTAAGAAAAATATTCATTTGGGTGATGACCACTTTGATCTCA 1264  
QY 1098 GAAAGATTCATCCCTAGTATACAAATTTGTTTATGACTTACATGCTGAGCCCTCTT 1157  
DB 1265 CACTGAATCTATTTGCCAACAATCCAGATTTGTTTATGACTTACATGCTGAGCCCTTAT 1324  
QY 1158 CCGGGAATGGGCCCATTTTCAACGGGTAAACAGCACCTGTGAGAACATGCTGGCCACT 1217  
DB 1325 TACAGAAATGGGCCAGGTTTTC--CAATACAGCTATCCAGACAAATGCTTGGACAG 1381  
QY 1218 CGCACACAAAGGCCCGATGGAAGAGCTGTGCCAGGACAGCAAGAGGAGGCA 1276  
DB 1382 GGGGCTGAATTAAGCCAGCTGGAAGGAGCTGCAGAGAGAAAGTGCAGCTGAGAGACA 1440

RESULT 14  
ID AA88175 standard; cDNA; 3987 BP.  
XX AA88175:  
XX 14-DEC-2000 (first entry)  
XX  
XX  
DE PTM22 human glioblastoma cell insert nucleotide sequence SEQ ID NO:19.  
XX  
XX  
KW Detection; mammalian gene; yeast; microorganism; identification;  
KW phenotype; characteristic; dunce-like phosphodiesterase; PDE; Ras;  
KW Ras-related protein; genetic defect; hybridisation; probe; ss.  
XX  
OS Homo sapiens.  
XX Saccharomyces cerevisiae.  
XX  
XX US610025-A.  
XX  
XX 08-AUG-2000.  
XX  
XX 01-MAR-1994; 94US-0206188.  
XX  
XX 20-APR-1990; 90US-0511715.  
XX 19-APR-1991; 91US-0688352.  
XX  
XX (COLD-) COLD SPRING HARBOR LAB.  
XX  
XX Colicelli JF, Wigler MH;  
XX  
XX WPI; 2000-531664/48.  
XX  
XX P-PSDB; AAB20619.  
XX  
XX Novel isolated DNA encoding a mammalian cyclic nucleotide  
XX phosphodiesterase is present in plasmids pPDE46, pPDE43 or pPDE339 and  
XX is used to modify a genetic defect in a biochemical pathway in which  
XX cAMP participates  
XX  
XX Example 1: Column 81-84; 145bp; English.  
XX  
XX The present invention describes a purified and isolated DNA (I) which  
XX encodes a mammalian cyclic nucleotide phosphodiesterase and is an insert  
XX present in the plasmids pPDE46 (ATCC 69552), pPDE43 (ATCC 69551) or

CC pPDE339 (ATCC 69550): The DNA molecules are used to modify, complement  
CC or suppress a genetic defect in a biochemical pathway in which CAMP  
CC participates and are also used as hybridisation probes. The present  
CC invention also describes methods for detecting mammalian genes encoding  
CC proteins which can function in microorganisms, particularly yeast, to  
CC modify, complement, or suppress a genetic defect associated with an  
CC identifiable phenotypic alteration or characteristic in the  
CC microorganism. AA88162 to AA88218 and AA89614 to AA820640 represent  
CC sequences used in the exemplification of the present invention.

XX  
SQ Sequence 3987 BP; 1137 A; 803 C; 817 G; 1222 T; 8 other;

Query Match 37.0%; Score 500.6; DB 21; Length 3987;  
Best Local Similarity 62.9%; Pred. No. 2.9e-146;

Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

QY 18 TCAGAGGTGTGGGCAATCTTGTGAGAACCCCGATCAGAAATGCCAAATGTGTTGCAT 77  
DB 185 TCAGAGGCGTGGAGCTATTCTTATGACAGTCTGTGATCAGACTGCATTAATGATTTGTAT 244  
QY 78 GCTGGAGATATACGACTAAGGGGTGACAGCGGGGTTGCTGCTGAACGCCGTGCTCTTA 137  
DB 245 GCTAGAGATGATGCTGTGTAAGCGGACGAGATTTGAATCAAGAAAGAGGTTCTCA 304  
QY 138 CCCATTGATGACTCCGCTACTTACAGTACATCATCAGGAGGAGATTGGACCA 197  
DB 305 CCCATATATGTTTTCGATTTTCCACTCTCAATCTGAATTTGAATGTCTGCTCTGC 364  
QY 198 GAAAAGGTGAAAGACATTAAGCTTTTCMAAGATCTTCATGTCATCAAGCTGCTCG 257  
DB 365 AAGGATATACAGAGGCTCTAAGTTTCCAGGATATCTTAGTCTTCAGGCTTTTGG 424  
QY 258 TGGATTAATACCAAGCCCTCTGCACTGCTGGATGAAGTACCTTTGGACAGCAAG 317  
DB 425 TGGTACTGGGTTTCAAAATTCCTTAACATTTTGAATGATTTAATGAACCAACCA 484  
QY 318 GCATATGCTCTCCAAAGTGGAGATGGATTTTGATCTTTCTGTGTGATGGCTGAC 377  
DB 485 GGTGATGCTGGAAAAAGTTGGAATTTGATTTGATTTCTTATTTGATGATGACTAAC 544  
QY 378 AAATGAAACAGCTGTGAACACCTGTTGTCACCTTTCAATACCATGAGCTATTC 437  
DB 545 AAATGAAATAGTCTAGTAAGCTTAACCTTCAATTTAGTCTCAATGATTAATTA 604  
QY 438 CCATTTCAAGTATGATGCTGACCTTACACCGATTTTATGATGCTTCAAGAGATTA 497  
DB 605 GTACTTCAATTTAGTATGATGAACCTTGTAGATTTTATGATTTCAAGAGATTA 664  
QY 498 CCACAGCCAAACCCGATACCAATGCTGTTCACGAGCGAGTCACCCAGGCAATGCA 557  
DB 665 CCACAGTCAAAATCTTACCATTAAGCAGCTCCAGCTGCGATGTTACTGAGGCCATGCA 724  
QY 558 CTGTAACCTGAAAGAGCCAAAGCTTCCAGCTTCCACGCTTGGACATATGCTTGG 617  
DB 725 CTGTACTTAAGGAACCTTAAGCTTCCCAATTCGTAACCTTGGGATATCTTGCTGAG 784  
QY 618 ACTGCTGGTGGAGAGCAGACATGCTGACCAACGAGGGGTGAACCAACCATTTTGT 677  
DB 785 CTTAATGTGAGTGCACATGATGTGATCATCCAGGTGTTAATCAACCTTCTTAT 844  
QY 678 AAAAATCAACCACTCTGCAACCTATATGATAATGATGCTGCTGAGAGATCATCA 737  
DB 845 TAAATCAACCTTACTTGGCAACTTATACAGAAATACCTAGTACTGGAATATCACA 904  
QY 738 CTGGGATCTACAAATGAGCTTCCAGATCAAGGCTTCTGCTCATTTGCCAAAGA 797  
DB 905 CTGGAGATCTGACGTGGCTTATGAGAAATACAGCTTATCTCATCTCCATTAGA 964  
QY 798 AATGACAGGATATGAAACAGCAGCTGGCTTGTGATCTTGGCAACGATCAACAG 857  
DB 965 AAGCAGGCAACAAATGAGACACAGATAGTGTCTCTGATACAGCCAGACAGATGCTG 1024  
QY 858 GCAGATGAATTTTACACAGATGAAGCTCACTCCACATTAAGACTGGA 917

DB 1025 CCAGATGATGATCTGTCTTTGTTAGTCCATTTGGATATGAGTATTTATGCTTACA 1084  
QY 918 GGATGACAGGACAGGACCTTTATGCTTACAGATGCCCTTGAAGTGTGACATTTGCA 977  
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## RESULT 15

AA526872  
ID AA526872 standard; cDNA; 2731 BP.

XX AA526872;

DT 07-NOV-2001 (first entry)

XX Human cDNA encoding a novel secreted protein, SEQ ID 64.

XX Human; immunosuppressive; antiarthritic; ss; antineumatic;  
KW cytototoxic; cardiant; vasotropic; cerebroprotective; nootropic;  
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
KW vulnery; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischaemia; angiodenesis;  
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.

OS Homo sapiens.

PN WO20015441-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01320.

XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
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 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 (HUMA-) HUMAN GENOME SCI INC.  
 Rosen CA, Barash SC, Ruben SM;  
 WPI: 2001-476223/51.  
 P-PSDB: AAU16967.  
 Novel polypeptides and polynucleotides useful as diagnostic reagents to  
 diagnose diseases or disorders associated with aberrant expression or  
 activity of polypeptides, for treating blood clotting disorder,  
 haemophilia  
 Claim 1; SEQ ID No 64; 601pp; English.  
 The invention relates to isolated nucleic acid molecules and their  
 encoded secreted proteins. The nucleic acids and proteins are used to  
 prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 rabbits, goats, horses, cats, dogs, chickens or sheep. They  
 are also used in diagnosing a pathological condition or susceptibility  
 to a pathological condition. Antibodies to the proteins can also  
 be used in alleviating symptoms associated with the disorders and in  
 diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
 immunosorbant assays (ELISA). Disorders which are diagnosed or treated  
 include autoimmune diseases e.g. rheumatoid arthritis,  
 hyperproliferative disorders e.g. neoplasms of the breast or liver,  
 cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders



CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
CC and ocular disorders e.g. corneal infection, and many other  
CC disorders listed in the specification. The polypeptides can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. The present

Query Match 34.3%; Score 463.6; DB 22; Length 2731;

Best Local Similarity 63.5%; Pred. No. 1e-134;  
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QY 198 GAAAAAGTGAAAAAGCTATTAAGCTTTCAAGATCTTCATGATCAGTCAAGGCTGCTCG 257  
DB 339 AAGGATATCAGAGAGCTACTAAGTTTCCAGCGATATCTTAGATCTTCAAGCTTTTTCG 398  
QY 258 TGGAAATTAACCAAGCCCGCTGACCTGCTGAGTGAAGACTACCTTGGAGAACAG 317  
DB 399 TGGTACTGGCGTTCAAAATTCCTAAACATTTTGAATGATTAATGACACAGCCAA 458  
QY 318 GCATATGCTCTCCAAAGTGGGAATGTGGATTTTGACATTTTCTGTTGATGCTTGAC 377  
DB 459 GTGTATGCTGGAAAAAGTTGGAATTTGGAATTTTGTATCTTCTATTTGATAGACTAAC 518  
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: em\_gss\_dln:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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LOCUS  
DEFINITION  
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(pgtrn) Gallus gallus cDNA clone pgtrn.pk001.a4 5' similar to  
g119506959.ref|NP\_061818.1| phosphodiesterase 7B [Homo sapiens]  
g113641697.ref|XE\_004434.2| phosphodiesterase 7B [Homo sapiens]  
g114781693.ref|XP\_050446.1| phosphodiesterase 7B [Homo sapiens]  
sp|O9NP56|CN7B\_HUMAN CAMP-SPECIFIC 3',5'-CYCLIC PHO, mRNA sequence.  
ACCESSION  
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VERSION  
BM439710.1 GI:18470485  
KEYWORDS  
EST.  
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Chicken.  
ORGANISM  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Phasianinae; Gallus.  
1 (bases 1 to 586).  
REFERENCE  
Cogburn,L.A. and Nys,Y.  
ESTs from Normalized Chicken Reproductive Tract cDNA library-  
University of Delaware and INRA, Tours-Poultry Unit Project  
Unpublished (2002)  
JOURNAL  
Contact: Larry A. Cogburn  
University of Delaware  
Townsend Hall, Newark, DE 19717, USA  
Tel: 302-831-1335  
Fax: 302-831-2822  
Email: cogburnudel.edu, www.chickest.udel.edu.  
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/lab\_host="E. coli EMD10B"  
 /note="Vector: PCWSPORT6; Library made from three total  
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 from 5'-end"

BASE COUNT 150 a 152 c 130 g 152 t 2 others  
 ORIGIN

Query Match 32.3%; Score 436.6; DB 10; Length 586;  
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 502 AGCCAAAGCCGATATCAATGCTGTGACAGCGAGCGAGTCAAGCGATGACATG 561  
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 436 AGCCAGAAAGCCGATATCAATGCTGTGACAGCGAGTCAAGCGATGACATG 495  
 562 TACCTGAAGAGCCAAAGCTTGGCAGTTCCTCAAGCGCTGAGATCAATGCTTGAGATG 621  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 496 TATCTAAGGAGGCCCAAGCTTGGCAGTTCCTCAAGCGATGACATGCTTGAGATG 555  
 622 CTGGCTGACAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 652  
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 556 CTGGCTGACAGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 586

RESULT 2  
 LOCUS B038504 628 bp mRNA linear EST 07-DEC-2001  
 DEFINITION B038504 NIBB Mochii normalized Xenopus neurula library Xenopus  
 laevis cDNA clone X1043K10 5', mRNA sequence.  
 ACCESSION B038504  
 VERSION B038504.1 GI:17405461  
 KEYWORDS EST.  
 SOURCE African clawed frog.  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 Xenopodinae; Xenopus.  
 1 (bases 1 to 628)  
 Kitajama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara  
 Y.,  
 Expressed genes in X. laevis embryo  
 Unpublished (2001)  
 JOURNAL  
 COMMENT Center For Genetic Resource Information

National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshin@genes.nig.ac.jp.  
 Location/Qualifiers

FEATURES  
 source 1..628  
 /organism="Xenopus laevis"  
 /db\_xref="taxon:8355"  
 /clone="X1043K10"  
 /clone\_1id="NIBB Mochii normalized Xenopus neurula  
 library"  
 /tissue\_type="whole embryo"  
 /dev\_stage="stage 15"

BASE COUNT 182 a 136 c 137 g 173 t  
 ORIGIN

Query Match 28.0%; Score 378.8; DB 10; Length 628;  
 Best Local Similarity 79.9%; Pred. No. 1.3e-97;  
 Matches 446; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

20 AGAGGTGGCGAATCTTGTGTAAGAACCCGATCAGATGATGCCAAATGTTTGATGC 79  
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 71 AAGGTGTGGAGAAATCTCATTTTGTATTAACCTGACCAAGAAATGTTTGATGCATGC 130  
 80 TGGAGATATACGACTAAGGGGTACAGACGGGGTTCGTTGTTGAACGCCGCTGCTACC 139  
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 131 TAGGAGATCTAGAGTGAAGAAATGTTCCAGCAGGGGTTCTCTCAGAACGCCGTGTTCAATACC 190  
 140 CATTCATGATCTCCGCTACTTAACAGTACATCACTCAGGGAGATTGGACCAAGA 199  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 191 CTTTATGATTTCCGCTCTTCATATATACATCACTCAGGAGAAATGCGCACTAAGA 250  
 200 AAAAGTGAAGAAAGACTATTAACTTTCAAGATCTTCATGATGATCAAGGCTGCTGATG 259  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 251 AGAAGTGAAGAAAGACTATTGAATTCAGAGATATTTTCATGATGATCAAGGCTGCTGATG 310  
 260 GAATTTATCAGACAGCCCTCTGACCTGCTGATGATGAAGAAAGTACTACTTGAGCAAGCAAGGC 319  
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 311 GAATTTGTCACAGAGCTTCTGACCTGTTGATGATGAAGAAAGTACTACTTGAGCAAGGCTGCGGG 370  
 320 ATATGCTCTCCAAAGTGGGAATGTGGATTTTGAATTTCTTGTGATGCTGTGACAA 379  
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 371 ATATGCTATCTAAAGTGGGAATGTGAATTTTGACATCTTCTGTTGATGCTGTGACAA 430  
 380 ATGGAAGAGCCGTGTGATCACTGTTGTGCACTCTTCAATACCAGTGAATGATTCACG 439  
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 431 ACGGTAAACGCTTAGTTAGTTATGTTGCAATGTTTAAATGTCACAGGGCTTATTCATC 490  
 440 ATTCAAGTTAGATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 499  
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 491 ACTTTGAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550  
 500 ACAGCCAAAGCCGATATCAATGCTGTGACAGCGAGCGAGTCAAGCGATGATGCCATGCTACT 559  
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 551 ATAGCCAAAGCCGATATCAATGCTGTGACAGCGAGTCAAGCGATGATGCCATGCTACT 610  
 560 GCTACCTGAAGAGCCAA 577  
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 611 GCTACCTGAAGAGCCAA 628

RESULT 3  
 LOCUS B164845 786 bp mRNA linear EST 12-SEP-2001  
 DEFINITION B03278377.1 NIH\_CGAP\_Mem3 Mus musculus cDNA clone IMAGE:5318514 5',  
 mRNA sequence.  
 ACCESSION B164845  
 VERSION B164845.1 GI:15562651  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 786)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-rt@mail.nih.gov](mailto:cgapbs-rt@mail.nih.gov)  
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at:  
<http://image.llnl.gov>  
Plate: L1AM1807 row: j column: 19  
High quality sequence stop: 775.  
Location/Qualifiers

FEATURES  
source 1..786  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5318514"  
/clone\_lib="NIH-CGAP\_Mam3"  
/tissue\_type="tumor, gross tissue"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: this is a NCI-CGAP library."

BASE COUNT 218 a 166 c 167 g 235 t  
ORIGIN

Query Match 25.1%; Score 340; DB 10; Length 786;  
Best Local Similarity 65.7%; Pred. No. 2,1e-86;  
Matches 510; Conservative 0; Mismatches 265; Indels 1; Gaps 1;

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QY 107 CGGGGTCGTCGCTAAGCCGCTGCTCTA-CCCATTCATGACTCGCGCTACTTAAC 165
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Db 7  CGTGGGTTGAACAAGAAAGAGGTTCCCATCGCTACATGACTCGTATTTTTCAC 66
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 166 AGTACACATACCTCAGGAGATGGACCAAGAAAGTGAAGAAAGACTATTAGCTTT 225
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 67 TCTCATTCGACATGGAACATCATCTCCGCCAGAACATCAGAAGTTACTTAAGTTTC 126
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QY 226 CAAGATATCTTCATGATCAAGGCTGCTCGTGAATTATTAACAACAGCCCTCTGCAC 285
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Db 127 CAGCGATATCTCAGATCTCAGAGTTTTCGCGGTCACAGATTGTGATCTCTAGAC 186
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QY 286 CTGCTGATGGAAGTACTACCTGGACAAAGCATATGCTCTCCAAAGTGGGATGTGG 345
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Db 187 ATTTAGATGAGATTTGAATGACAGCAAGTATGCTGGAAGAAAGTTGGAATGTG 246
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QY 346 GATTTTGACATTTCTGTGATGCTGTGACAAATGGAACAGCGCTGGTACACATGTTG 405
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Db 247 AATTTGATATCTCTCTGTTGATAGACTACAAATGGAAGTAAAGTCTAGAGCTTAAC 306
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QY 406 TCCACCTCTCAATACCCAGTCACTCAATCCATTTCAAGTATGATGTGACCTTA 465
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Db 307 TTTCAATTTATAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 366
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QY 466 CACGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525
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Db 367 GGTGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
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QY 526 GTTTCAGGAGCGAGTACCCAGCCATGCACTGCTACCTGAAAGAGCAAGCTTGCC 585
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Db 427 GTTCATGCTGAGAGCTTACTAGGCCATGCACTGTTACTTAAGAACTTAAGCTTGCC 486
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QY 586 AGCTTCTCAGCGCTCTGAGACATCATGCTGTGACTGTGGCTGACAGACACAGATGTG 645
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Db 487 AGTTCTGACAGCTCTGGGATATCTTGTGAGTTTAATTGACGCGCACATCAGATCTG 546
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QY 646 GACCACCAGGCGTGAAACCAGCCATTTTGTATTAATAACCAACCAGATCTGCAACCTA 705
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Db 547 GATCACCCAGGCTGTTATATACAGCCGTTTCTTATTAACCAACCATTAATATACACTTAA 606
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QY 706 TATCAGAAATATGCTGTGCTGAGATCAATCAATCACTGCGCATCTACATTTGGATCTTGA 765
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 607 TACAGAAATCTCAGTCTGAGATACACATCGAGATCTGACAGTGGCGCTTGTAA 666
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QY 766 GAATCAGGCTCTGCTCATTTTGGCAAGAAATGACACAGATATTAACAGCAGCTG 825
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 667 GAATCTGTTTGTCTCACACTTGGCAAGAAACAGCAGAGATGAGAGCTCAGATA 726
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 826 GGCCTCTTATCTTGGCAACAGATCAACAGCAGCAATGATTTTGGACAGATT 881
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Db 727 GGTGCTTATATTTAGCCAGATATCAGTCCGCCAGACGATACCTGTCCTGTT 782
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RESULT 4  
AM851659 382 bp mRNA linear EST 19-MAY-2000  
LOCUS  
DEFINITION MR2-CT0222-261099-003-h11 CT0222 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AM851659  
VERSION AM851659.1 GI:7947176  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 382)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,  
M.J., Soares,F., Brentani,I.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
2020263  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL:  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=et2-MR2-CT0222-261>)  
099-003-h11&t3=1999-10-26&t4=1)

Seq primer: puc 18 forward  
High quality sequence start: 21  
High quality sequence stop: 381.  
Location/Qualifiers

FEATURES  
source

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/db\_xref="taxon:9606"  
/clone\_lib="CT0222"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 112 a 93 c 109 g 66 t 2 others  
ORIGIN

Query Match 24.8%; Score 336.2; DB 9; Length 382;  
Best Local Similarity 98.4%; Pred. No. 1.1e-85;



	expressed	in HT1080	under normal	circumstances.
BASE COUNT	230 a	180 c	212 g	265 t
ORIGIN				2 others

Query Match	22.6%	Score 305.8	DB 10	Length 889
Best Local Similarity	91.8%	Pred. No. 1.6e-76		
Matches 367	Conservative	0	Mismatches 28	Indels 5
				Gaps 4

QY	316	AGGATATGCTCCTCCAAAGTGGAGTGGGATTTTGGACATTTCTGTGTTATGACCTTG	375
Db	724	AAGCAATGCTCTTCAAAAGTGGAAATGTGGA-TTTGCCATTTTCTGGTTTATGCTTT	666
QY	376	ACAAATGGA--AAGACGCTGGTACACGTGTTGTGCACCTCTTCATATACCATGACCTCA	433
Db	665	ACCAAAATGGTTACAAAGCTGGGGATCCATGNTGTGCACACTCTTCAAAACCCAGACTTCA	606
QY	434	TTCCACCAATTC-AGSTTATGATATGCTGACCTTACA-CCGATTTTAAATGTCATGTTCAAGA	491
Db	605	TTTCACCAATTTCAAAAGTTATGATATGCTGACCTTACACCCGATTTTAAATGTCATGTTCAAAA	546
QY	492	AGATTTACCAACGCAAAACCCGTATACAAATGCTTACAGACGACGAGCTACACCAGGC	551
Db	545	AGATTTACCAACGCAAAACCCGTATACAAATGCTTACAGACGACGAGCTACACAGGC	486
QY	552	CATGCACGTCTACCTGGAAGAAGCCAAAGCTTGCCACGTCTCTACAGCCTCTGGACATCAT	611
Db	485	CATGCACGTCTACCTGGAAGAAGCCAAAGCTTGCCACGTCTCTACAGCCTCTGGACATCAT	426
QY	612	GCTTGGACTGCTGCGCTGACGACGACACAGATGTGGACCAACCCAGGAGGTGAACACGCAAT	671
Db	425	GCTTGGACTGCTGCGCTGACGACGACACAGATGTGGACCAACCCAGGAGGTGAACACGCAAT	366
QY	672	TTTGATTAATACTACCAACACTCTTGCAAACTATATAG 711	
Db	365	TTTGATTAATACTACCAACACTCTTGCAAACTATATAG 326	

RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT															
BF614359	BF614359	673 bp mRNA linear EST 14-DEC-2000	de05f03.y1	Wellcome CRC PRN3 oocyte Xenopus laevis cDNA clone IMAGE:3437308 5' similar to SW:CN7A.HUMAN Q13946 HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE ; mRNA sequence.	BF614359	BF614359	GI:11786903	EST	African clawed frog.	Xenopus laevis	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.	1 (bases 1 to 673)	Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Rittler,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.	Mashu Xenopus EST project, 1999	unpublished (1999)	Other ESTs: de05f03.x1	Contact: Sandy Clifton, Ph.D.	Washu Xenopus EST project, 1999	Washington University School of Medicine	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	Tel: 314 286 1800	Fax: 314 286 1810	Email: est@watson.wustl.edu	Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center	clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LNL at: info@image.lnl.gov	Seq primer: -40RP from Gibco	High quality sequence stop: 501.

FEATURES	Location/Qualifiers
source	1. .673

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/clone="IMAGE:3437308"
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/tissue_type="oocyte"
/lab_host="IDH10B (phage-resistant)"
/notes="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library was constructed
by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon
(Wellcome/CRC Institute)."
BASE COUNT      191 a      148 c      165 g      169 t
ORIGIN
Query Match      21.7%;   Score 293.4;  DB 10;  Length 673;
Best Local Similarity 65.9%;   Pred. No. 4.9e-73;
Matches 442; Conservative 0; Mismatches 226; Indels 3; Gaps 1

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LOCUS	DEFINITION	BE782968	930 bp	mRNA	linear	EST 20-OCT-2000
QY	599	CTTGGACATCATGCTTGGACGTGCTGGGCTGCAGCAGCACACGATGTGGACACCAAGGGG	658			
Db	3	CTTGGATATCTCGTGGGCTTGATTGCAAGCTGCACACACGATTTGGATCATCCGGTG	62			
QY	659	TGAACACGCCATTTTGTGATAAAACTAAACACACCATCTTGCAAACCTATATACGATATGT	718			
Db	63	TAAACACTCTTGGTATATAAAAAACAAACCACTACTTACGACTTTATACAGAAATACCT	122			
QY	719	CTGTGCTGGAGATATCATCTAGTGGCATCTACATTTGGCATGCTTGGAGATATCAAGCTTC	778			
Db	123	CAGATTTAGAGAACCAACCACTGGAGATACAGCATGGGGTCTGTTGGCTGTAATGGGGTTCT	182			
QY	779	TTGCTCATTTGGCCAAAGGAAATGACACAGATATTGAACAGAGCTGGGCTCCTTGATCT	838			
Db	183	TTTCACACTTTGCATATTAGAGGAGACACACATGMAAAGCCAGTTGGGCTCTATCATTC	242			
QY	839	TGGCACAGACATCAACAGCGCAGAAATGAAATTTTGAACAGATTGAAGCTCACCTCCACA	898			
Db	243	TTGCTACAGATATAGTGGCCAAATGAATACCTCTCGCAGTTTGAATCTTCCGGATA	302			
QY	899	ATTAAGACTTAAAGATGGAGAGATGCACAGACAGCAGCTTTATGCTTCGATCGGCTTGA	958			
Db	303	GAGGAGACTTATAGCTTAGACACAACGCCACTGACAGACTCTTATVCTGCAGATGGCTCTGA	362			
QY	959	AGTGTGCTGACATTTGCAATCCTTTAGAAATGTGGAGATGAGCAAGCAGTGGAGTAA	1018			
Db	363	AGTGTGCGGATATATGTAATGTAATCCTCCCTACTCTGGGAGCTGATGAACAGTGGAGTAA	422			
QY	1019	GGGTCTGTGAAGAAATTTTCAACAGGCAAGGTGAACCTTGAACAGAAATTTGAACTGGAATCA	1078			
Db	423	AAGTGCACAGAAAGATGCTTTTATCAAGGCGAGTGTGAAGCAAAATTAACATGAGATGCA	482			
QY	1079	GTCCCTTTGTAAATCAACAGAAAGATTCATCCCAATATCAAAATGGTTCATGAGGT	1138			
Db	483	GTCCACTGTGCATCGGATATCATGAAATATAGCCAAATATCCAGATGGTTCATTAACGT	542			
QY	1139	ACATGTGTGAGACCGCGTCTTCGCGAGTGGGCCCATTTTACGGGTAAACACACACCTGTCCG	1198			
Db	543	ACCTGTGTGAGCGCATTTGGTTGAGAGATGGGGCCGGTTCA---GTAAACACAGGCTGTCC	599			
QY	1199	AGAACATCTGTGGGCGACCTCGCACACAAACAAAGGCCCATGTGGAAGAGCCTGTGGCCAGGC	1258			
Db	600	AGACCATCTCTGTGCCACGTATGATCATATAGAGCCACAGGCTGAACAGAGATGTGCATGAGC	659			
QY	1259	AGCACAGAACG 1269				
Db	660	GCTCGAGCAGC 670				

RESULT 8			
BE782968			
LOCUS	BE782968	930 bp	mRNA
DEFINITION	60147212to1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3875546 5',	linear	EST 20-OCT-2000

mRNA sequence.  
 BE782968  
 BE782968.1 GI:10204166  
 EST.  
 VERSION  
 BE782968.1  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 930)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM9634 row: 0 column: 03  
 High quality sequence stop: 678.  
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 Average insert size 1.75 kb. Library constructed by Life  
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 QY 202 AAGGTGAAGAGCTATTACCTTTCACCAAGATCTTCATCCATCAAGAGCTGCTGTGA 261  
 Db 9 AATATCGAAGAGCTATTACCTTTCACCAAGATCTTCATCCATCAAGAGCTGCTGTGA 68  
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 QY 322 ATGCTCTCAAGAGCTATTACCTTTCACCAAGATCTTCATCCATCAAGAGCTGCTGTGA 381  
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QY 682 ACTAACCCATCTTGCACCAACCTATATCAGATATGCTGTGAGATCAGTCTGG 741  
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 DEFINITION  
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 ACCESSION  
 BG863353  
 VERSION  
 BG863353.1 GI:14213891  
 KEYWORDS  
 EST.  
 SOURCE  
 house mouse.  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 599)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Lotar Hennighausen Ph.D., Priscilla Furth  
 Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
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 Reference for transgenic model: Li et al., Cell Growth and  
 Differentiation 7, 3-11 (1996). Note: this is a NCI\_CGAP  
 Library."  
 BASE COUNT 168 a 122 c 123 g 186 t  
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 Best Local Similarity 69.0%; Pred. No. 5.9e-70;  
 Matches 401; Conservative 0; Mismatches 179; Indels 1; Gaps 1;  
 QY 190 GGCACCAAGAAAGCTTAAAGCTTTCATGATGATGATGATGATGATGATGATGATG 249  
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Oy	250	CTGCTGCGGAATTAATACCAACAGCCCCCTCGACCCGCTGGAGATGAAGACTACTCTTGA	309
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Oy	310	CAAGCAAGGCATATATGCTCTCCAAAGTGGGAATGTGGAGATTTTGACATTTCTCTGTTGAT	369
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Oy	670	TTTTTGAATAAAAAATCAACACCATTTTGCACCAACCTATATTCAGTAATATCTGTGGAG	729
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ACCESSION	601784341F1	NCI_CGAP_Lu30	Mus musculus	CDNA clone	IMAGE:4011946 5',
VERSION	BF134357				
KEYWORDS	BF134357.1	GI:10973397			
SOURCE	EST.				
ORGANISM	house mouse.				
	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	1 (bases 1 to 929)				
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>				
	Tissue Procurement: Gilbert Smith, Ph.D.				
	CDNA Library Preparation: Life Technologies, Inc.				
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: NCI-CGAP clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNLN at:				
	<a href="http://image.lnl.gov">http://image.lnl.gov</a>				
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Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT      279 a      216 c      213 g      221 t
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Query Match	19.6%	Score 265.6	DB 10	Length 929
Best Local Similarity	66.9%	Pred. No. 5.8e-65		
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Db 5	TGATTCAAGAAGATTACACAGTCAAATTCCTTACCACATGCAATGCTGTGACAGC	64		
QY 542	TCACCCAGGCCATGCACTGCTTACCTGAAAGCCAAAGCTTGCCACGCTTC	601		
Db 65	TTACTCAGGCCATGCACTGTTACTTAAAGAACTTAAGCTTGCCAGTTCTGCACTCCTT	124		
QY 602	TGGAATCATGCTTGGACGCTGGCGACGACACAGCATGAGGACCAACCCAGGGGGA	661		
Db 125	GGGATATCTTGCTGAGTTTAAATGACCGCCACTACCATCTGGATTCACCCAGGTGTA	184		
QY 662	ACCAACCAT-TTTTGATTAATACTAACCCACATCTTGCAACCTATATAGAAATGTCT	720		
Db 185	ATCAGCCGTGTCTTATTAATAACCAACATATCTGCAACCTTATACAAAGAAATCTCA	244		
QY 721	GTGCTGAGAAATCATCTGCGCATCTACAAATGGCATGCTTCGAGAAATCAAGGCTTCT	780		
Db 245	GTCCTGGAGATCAACCCTGGAATCTGCAAGTGCGTTTGAAGAGAAATC--TGATTGTT	302		
QY 781	GCTCATTTGCCAAAGGAATGACACAGAAATGAAACACACAGCTGGGCGCTTGATCTTG	840		
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QY 841	GCAACAGACATCAACAGGCGAAATGAATTTTGTGACCAATGGAAGCTCACCTCCACAT	900		
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QY 901	AAACACTTAAGACTGGAAGATGCACAGGACAGGCACTTTATGCTTCAGATGCCCTTGAAG	960		
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Db 482	TGTCTGTATTTTGTAACTCATGTCGAACTGGGAATTAAGCAAGACGTGGCGGTGAAA	541		
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QY 1078	AGTCTCTTTGTATTAACAAGAAAGATTCCTATCTAGTATTAACAATTTGGTTTCAATGAGC	1137		
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DEFINITION	BE030578	538 bp	mRNA	linear	EST 09-JUL-2000
ACCESSION	128655	MARC	1P1G	Sus scrofa	cDNA 5', mRNA sequence.
VERSION	BE030578				
KEYWORDS	BE030578.1	GI:8325587			
SOURCE	EST.				
ORGANISM	Sus scrofa				
	Pig.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				

REFERENCE 1 (bases 1 to 538)  
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,  
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.,  
and Keefe,J.W.  
TITLE Design and use of two pooled tissue normalized cDNA libraries for  
EST discovery in swine  
JOURNAL Unpublished (2000)  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -mnscore 18  
and -mismatch 12 options.  
PCR primers  
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BACKWARD: GCTTCCAGTCACGACG  
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Library made from pooled tissue from day 11, 13, 15, 20,  
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Best local similarity 68.5%: Pred. No. 5.6e-65;  
Matches 366; Conservative 0; Mismatches 168; Indels 0; Gaps 0;  
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DB 5 CATGATTAATGATGATCTTCCATTTAGATATGATAAATCTGATTTTGTATG 64  
OY 484 GTTCAAGAATTAACACAGCAAAACCGTATACAAATGCTGTTCCAGCAGCGAGTC 543  
DB 65 ATTCAAGAATTAACACAGCAAAACCGTATACAAATGCAATGCAAGCTGCAAGTCG 124  
OY 544 ACCGAGGCATGACCTGCTACTGTAAGAGAGCAAAAGCTTGCCAGCTTCTCAGGCTGTG 603  
DB 125 ACTCAGGCATGACCTGTTACTTAATAAGAACTAGCTTGCAGTTGTACTCTTGG 184  
OY 604 GACATCATCTTGGATGCTGGCGTGCAGCAGCAGCAGATGTCAGACCCAGGGGTGAAC 663  
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OY 664 CAGCCATTTTGAATAAAATCAACACCATCTTGCAAAACCTATATCAGAAATATGTCGTG 723  
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OY 904 GACTTAAGACTGAGAGATGACAGAGACGAGCACTTATATCTTCAGATGCTGCTG 957  
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DEFINITION B1656808 1137 bp mRNA linear EST 12-SEP-2001  
LOCUS 603281492P1 NIH\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:5325767 5',  
mRNA sequence.  
ACCESSION B1656808  
VERSION B1656808  
KEYWORDS B1656808.1 GI:15571044  
SOURCE EST.  
ORGANISM house mouse.  
Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1137)  
AUTHORS NIH-MGC  
TITLE NIH-MGC http://mgi.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
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Average insert 2.5 Kb. Library constructed by Life  
Technologies, catalog # 12018-016. Investigators providing  
samples: Lothar Hennighausen/Priscilla Furth, NIH  
Reference for transgenic model: Li et al., Cell Growth and  
Differentiation 7, 3-11 (1996). Note: this is a NIH\_CGAP  
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Best local similarity 69.0%: Pred. No. 8.3e-65;  
Matches 363; Conservative 0; Mismatches 163; Indels 0; Gaps 0;  
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DB 1 ATGAGTATGATGATGATCTTCCATTTAGATATGTAAGAACCTGCGTTTATGATGA 60  
OY 485 TTCAAGAATTAACACAGCAAAACCGTATACAAATGCTGTTCCAGCAGCGAGTC 544  
DB 61 TTCAAGAATTAACACAGCAAAACCGTATACAAATGCTGTTCCAGCAGCGAGTC 120  
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QY	845	CAGACATCAACAGCGCAGATGATATTTTGTACCCAGATTTGAAGCTTCACCTCCACATAAAG	904
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ACCESSION	BB664044		
VERSION	BB664044.1	GI:16497798	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 632)		
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,T., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.		
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Shuhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gs.riken.go.jp, url:http://genome-gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wag1,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanae,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome-gsc.riken.go.jp) for further details. e mouse tissues.		

FEATURES					
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		GAGGAGAGAGACGGCGCCCACTGCAGTTTATTTTTTTTAA 3'}			
		cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adaptor of sequence [5']			
		GAGGAGAGATTTCGAGTAATAAATTAATCCCCCCCCCCC 3'}. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."			
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Matches	281; Conservative	0;	Mismatches	32; Indels	0; Gaps
OY	1	ATGCTTGTTTAATGTTGAGAGGTGTGGCGAATCTTGTGTGAGAACCCGATCAGAT	60		
Db	320	ANGCTGTTGTTAATGTTGAGAGGTGTGGCGAAGTCTTGTGTGAGAGCCCTGAACAGAGT	379		
OY	61	GCCAAATGTGTTTCATGCTGGGAGATATACACTAAAGGGTCAGACGGGGTCTGCTCT	120		
Db	380	GTCAAATGTGTTTCATGCTAGAGATGTACACTAAAGGGGTCAACGGGGTCTCTGCC	439		
OY	121	GAAGCCCGGGGCTCTACCACATCATTTACCTTCCGCCCTACTTAACAATCAACATACCA	180		
Db	440	GAAGCCCGGGGCTCTACCACATCATTTACCTTCCGCCCTACTTAACAATCAACACACTCA	499		
OY	181	GGGAGATTGGCACCAAAAAAGGTGAAAAGACTATTAAAGCTTCAAGAATACTTCAT	240		
Db	500	GGGGAATTTGGCACCAAAAAAGGTGAAAAGACTGTTTAAGTTCCAAGAATACTTCAT	559		
OY	241	GCATCAGAGCTGCTTGTGGAATTTATACCACAGCCCTCTGCACCTCTGTGATGAGAC	300		
Db	560	GCATCTAGAGCCCTCTCGGGGATTTATACCGTAGCCCTCTGCACCTCTGTGATGAGAAC	619		
OY	301	TACCTTGGACAG 313			
Db	620	TACCTTGGACAG 632			
RESULT 14					
LOCUS	BE479018	319 bp	mRNA	linear	EST 28-AUG-2000
DEFINITION	163549 BARC 5BOV Bos taurus cDNA 5'				
ACCESSION	BE479018				
VERSION	BE479018.1	GI:3598551			
KEYWORDS	EST.				
SOURCE	COW.				
ORGANISM	Bos taurus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;					
Bovidae; Bovinae; Bos.					
1 (bases 1 to 319)					
Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and Wells,K.D.					
Mapping of Expressed Sequence Tags from a normalized bovine mammary					



Db 147 GCTGATATTGTAACCATGTCGACGTGGGAATTAGCAACAGTGGAGTGAAAAAGTA 88  
Oy 1024 TGTGAAGAATTCTACAGCAAGTGAAGTGAACCTGACAGAAATTGAACTGGAATCAGTCCT 1083  
Db 87 ACGGAGGAATTCTTCATCAAGAGATATAGAAAAAATATCATTTGGGTGTGAGTCCA 28  
Oy 1084 CTTGTAATCAACAGAGAAGATTCAT 1109  
Db 27 CTTTCGATCGTCACACTGAATCTAT 2

Search completed: October 27, 2002, 09:20:07  
Job time : 1739 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2002, 07:23:37 : Search time 61 Seconds  
(without alignments)  
20.030 Million cell updates/sec

Title: US-09-471-459a-9  
Perfect score: 61  
Sequence: 1 MSCLMERGE 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_032802:\*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
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6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
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13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
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15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	21	AAV93577
2	61	100.0	268	21	AAV93593
3	61	100.0	288	21	AAV93568
4	61	100.0	413	21	AAV93571
5	61	100.0	437	21	AAV93572
6	61	100.0	445	21	AAV93573
7	61	100.0	446	21	AAV93567
8	61	100.0	446	21	AAV93574
9	61	100.0	450	21	AAV93569
10	61	100.0	450	22	AAV93569
11	61	100.0	450	22	AAV93569

12	61	100.0	451	21	AAV93575	Amino acid sequenc
13	41	67.2	19	22	AAV85566	Human secreted pro
14	41	67.2	23	22	AAV85565	Human secreted pro
15	41	67.2	47	22	AAV85564	Human secreted pro
16	41	67.2	132	22	AAV00699	Human secreted pro
17	41	67.2	152	22	AAV11697	Human novel protei
18	41	67.2	154	22	AAV00702	Human novel protei
19	41	67.2	188	22	AAV85563	Human secreted pro
20	41	67.2	200	21	AAV71128	Human platelet Der
21	41	67.2	322	21	AAV71129	Human platelet Der
22	41	67.2	364	22	AAV12264	Human PR04345 poly
23	41	67.2	370	21	AAV48653	Human growth facto
24	41	67.2	370	21	AAV48653	Mouse growth facto
25	41	67.2	370	21	AAV96864	SEQ. ID. 37 from W
26	41	67.2	370	21	AAV71130	Human platelet Der
27	41	67.2	370	22	AAV63601	Human zveig14 polyp
28	41	67.2	370	22	AAV65602	Mouse zveig14 polyp
29	41	67.2	370	22	AAV85529	Human secreted pro
30	41	67.2	370	22	AAV85547	Human secreted pro
31	41	67.2	370	22	AAV00698	Human FCTR1 protei
32	41	67.2	370	22	AAV00700	Mouse FCTR3 protei
33	41	67.2	370	22	AAV00704	Human PDGFR protei
34	41	67.2	370	22	AAV00999	Human zveig14 prote
35	41	67.2	370	22	AAV60888	Human VEGF-G prote
36	41	67.2	370	22	AAV60895	Human VEGF-G prote
37	40	65.6	113	21	AAV10631	Human VEGF-X prote
38	40	65.6	113	21	AAV10632	Human VEGF-X prote
39	40	65.6	121	22	AAV74034	Synthetic protein
40	40	65.6	123	22	AAV74033	Synthetic protein
41	40	65.6	149	21	AAV10642	Human VEGF-X PDGF
42	40	65.6	227	21	AAV10637	Human VEGF-X prote
43	40	65.6	227	21	AAV10638	Human VEGF-X prote
44	40	65.6	318	21	AAV84558	A fragment of plat
45	40	65.6	339	21	AAV58438	Lung cancer associ

#### ALIGNMENTS

RESULT 1	
AAV93577	standard; Peptide; 11 AA.
XX	
AC	AAV93577:
XX	
DT	25-SEP-2000 (first entry)
XX	
DE	Amino acid sequence of a phosphodiesterase peptide fragment.
XX	
KW	Phosphodiesterase; PDE-XIV; enzyme.
XX	
OS	Synthetic.
XX	
PN	EP1018559-A1.
XX	
PD	12-JUL-2000.
XX	
PF	09-NOV-1999; 99EP-0308902.
XX	
PR	23-DEC-1998; 98GB-0028603.
XX	
PR	17-SEP-1999; 99GB-0022123.
XX	
PA	(PF12 ) PFIZER LTD.
XX	
PI	(PF12 ) PFIZER INC.
XX	
DR	Fidock M;
XX	
WPI	2000-433274/38.
XX	
PT	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
XX	useful for preventing diagnosing and treating diseases associated with
PT	inappropriate PDE-XIV expression and/or activity -
XX	

PS Disclosure; Page 4; 104pp; English.

XX AAY93576-90 represent fragments of a phosphodiesterase (PDE)-XIV enzyme.  
CC The peptide fragments can be used to construct a phosphodiesterase  
CC enzyme sequence from a formula of the invention. The phosphodiesterase  
CC polynucleotide and polypeptide may be used in the prevention, treatment  
CC and diagnosis of diseases associated with inappropriate PDE-XIV  
CC expression. For example, the polynucleotide be administered to treat  
CC diseases by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of PDE-XIV. They may also be used to study  
CC the expression and function of PDE-XIV polypeptides and their role in  
CC metabolism. The PDE-XIV polypeptides may be used as antigens in the  
CC production of antibodies against PDE-XIV and in assays to identify  
CC modulators (agonists and antagonists) of PDE-XIV expression and  
CC activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also  
CC be used to down regulate PDE-XIV expression and activity (i.e. the  
CC PDE-XIV gene and/or expression product may be used in the preparation  
CC of a composition for the treatment of a disorder associated with  
CC inappropriate PDE-XIV expression and/or activity and to screen for  
CC agents that can modulate PDE-XIV expression and or activity. The  
CC anti-PDE-XIV antibodies may also be used as diagnostic agents for  
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by  
CC enzyme linked immunosorbent assay (ELISA)).

XX Sequence 11 AA;

Query Match 100.0%; Score 61; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLMERGCE 11  
Db 1 MSCLMERGCE 11

RESULT 2  
AAY93593  
ID AAY93593 standard; Protein; 268 AA.

XX AAY93593;

DT 25-SEP-2000 (first entry)

XX Amino acid sequence of a human phosphodiesterase enzyme.

DE Phosphodiesterase; PDE-XIV; enzyme.

KW Homo sapiens.

XX EP1018559-A1.

XX 12-JUL-2000.

XX 09-NOV-1999; 99EP-0308902.

XX 23-DEC-1998; 98GB-0028603.

XX 17-SEP-1999; 99GB-0022123.

XX (PF12 ) PFIZER LTD.

PA (PF12 ) PFIZER INC.

PI Fldock M;

XX WPI; 2000-433274/38.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
XX useful for preventing diagnosing and treating diseases associated with  
XX inappropriate PDE-XIV expression and/or activity -

XX Disclosure; Page 87-88; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE) enzyme. The  
CC phosphodiesterase polynucleotide and polypeptide may be used in the

CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PDE-XIV expression. For example, the polynucleotide  
CC be administered to treat diseases by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of PDE-XIV. They may  
CC also be used to study the expression and function of PDE-XIV  
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides  
CC may be used as antigens in the production of antibodies against PDE-XIV  
CC and in assays to identify modulators (agonists and antagonists) of  
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and  
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression  
CC and activity (i.e. the PDE-XIV gene and/or expression product may be  
CC used in the preparation of a composition for the treatment of a disorder  
CC associated with inappropriate PDE-XIV expression and/or activity and to  
CC screen for agents that can modulate PDE-XIV expression and or activity.  
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for  
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by  
CC enzyme linked immunosorbent assay (ELISA)).

XX Sequence 268 AA;

Query Match 100.0%; Score 61; DB 21; Length 268;  
Best Local Similarity 100.0%; Pred. No. 0.026; 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLMERGCE 11  
Db 1 MSCLMERGCE 11

RESULT 3  
AAY93568  
ID AAY93568 standard; Protein; 288 AA.

XX AAY93568;

DT 25-SEP-2000 (first entry)

XX Amino acid sequence of a human phosphodiesterase enzyme.

DE Phosphodiesterase; PDE-XIV; human; enzyme.

KW Homo sapiens.

XX EP1018559-A1.

XX 12-JUL-2000.

XX 09-NOV-1999; 99EP-0308902.

XX 23-DEC-1998; 98GB-0028603.

XX 17-SEP-1999; 99GB-0022123.

XX (PF12 ) PFIZER LTD.

PA (PF12 ) PFIZER INC.

PI Fldock M;

XX WPI; 2000-433274/38.

XX N-PSDB; AAA46650.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
XX useful for preventing diagnosing and treating diseases associated with  
XX inappropriate PDE-XIV expression and/or activity -

XX Disclosure; Page 42-44; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The  
CC phosphodiesterase polynucleotide and polypeptide may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PDE-XIV expression. For example, the polynucleotide  
CC be administered to treat diseases by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of PDE-XIV. They may  
CC also be used to study the expression and function of PDE-XIV



CC polypeptides and their role in metabolism. The PDE-XIV polypeptides  
CC may be used as antigens in the production of antibodies against PDE-XIV  
CC and in assays to identify modulators (agonists and antagonists) of  
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and  
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression  
CC and activity (i.e. the PDE-XIV gene and/or expression product may be  
CC used in the preparation of a composition for the treatment of a disorder  
CC associated with inappropriate PDE-XIV expression and/or activity and to  
CC screen for agents that can modulate PDE-XIV expression and or activity.  
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for  
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by  
CC enzyme linked immunosorbant assay (ELISA)).

SQ Sequence 288 AA:

Query Match 100.0%; Score 61; DB 21; Length 288;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLMERGE 11  
Db 1 MSCLMERGE 11

RESULT 4  
AA93571  
ID AA93571 standard; Protein; 413 AA.

AC AA93571;

DT 25-SEP-2000 (first entry)

DE Amino acid sequence of a phosphodiesterase enzyme.

KW Phosphodiesterase; PDE-XIV; enzyme.

OS Synthetic.

PN EP1018559-A1.

PD 12-JUL-2000.

PE 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PF12 ) PRIZER LTD.  
PA (PF12 ) PRIZER INC.

PI Fldock M;

DR WPI; 2000-433274/38.

PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
PT useful for preventing diagnosing and treating diseases associated with  
PT inappropriate PDE-XIV expression and/or activity -

PS Claim 2; Page 55-57; 104pp; English.

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.  
XX The enzyme sequence is derived from a formula of the invention. The  
XX phosphodiesterase polynucleotide and polypeptide may be used in the  
XX prevention, treatment and diagnosis of diseases associated with  
XX inappropriate PDE-XIV expression. For example, the polynucleotide  
XX be administered to treat diseases by rectifying mutations or deletions  
XX in a patient's genome that affect the activity of PDE-XIV. They may  
XX also be used to study the expression and function of PDE-XIV  
XX polypeptides and their role in metabolism. The PDE-XIV polypeptides  
XX may be used as antigens in the production of antibodies against PDE-XIV  
XX and in assays to identify modulators (agonists and antagonists) of  
XX PDE-XIV expression and activity. The anti-PDE-XIV antibodies and  
XX PDE-XIV antagonists may also be used to down regulate PDE-XIV expression

CC and activity (i.e. the PDE-XIV gene and/or expression product may be  
CC used in the preparation of a composition for the treatment of a disorder  
CC associated with inappropriate PDE-XIV expression and/or activity and to  
CC screen for agents that can modulate PDE-XIV expression and or activity.  
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for  
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by  
CC enzyme linked immunosorbant assay (ELISA)).

SQ Sequence 413 AA:

Query Match 100.0%; Score 61; DB 21; Length 413;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLMERGE 11  
Db 1 MSCLMERGE 11

RESULT 5  
AA93572  
ID AA93572 standard; Protein; 437 AA.

AC AA93572;

DT 25-SEP-2000 (first entry)

DE Amino acid sequence of a phosphodiesterase enzyme.

KW Phosphodiesterase; PDE-XIV; enzyme.

OS Synthetic.

XX Key Location/Qualifiers

FT FH Misc-difference 12

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 16

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 18

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 20

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 29

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 38

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 55

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 58

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 113

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 140

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 167

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 305

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 347

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 376

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 388

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 401

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 415

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 419

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 423

FT /note= "any suitable peptide sequence or amino acid"

FT FT Misc-difference 425

FT /note= "any suitable peptide sequence or amino acid"

FT MISC-difference 428 /note- "any suitable peptide sequence or amino acid"  
 FT MISC-difference 430 /note- "any suitable peptide sequence or amino acid"  
 FT MISC-difference 433 /note- "any suitable peptide sequence or amino acid"  
 FT MISC-difference 436 /note- "any suitable peptide sequence or amino acid"  
 FT MISC-difference 436 /note- "any suitable peptide sequence or amino acid"  
 PN EPI1018559-A1.  
 PD 12-JUL-2000.  
 XX 09-NOV-1999; 99EP-0308902.  
 PR 23-DEC-1998; 98GB-0028603.  
 PR 17-SEP-1999; 99GB-0022123.  
 XX (PFI2 ) PFIZER LTD.  
 PA (PFI2 ) PFIZER INC.  
 XX Fldock M;  
 PI WPI; 2000-433274/38.  
 DR Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
 PT useful for preventing diagnosing and treating diseases associated with  
 PT inappropriate PDE-XIV expression and/or activity -  
 XX Disclosure; Page 58-60; 104pp; English.  
 PS The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.  
 CC The enzyme sequence is derived from a formula of the invention. The  
 CC phosphodiesterase polynucleotide and polypeptide may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PDE-XIV expression. For example, the polynucleotide  
 CC be administered to treat diseases by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of PDE-XIV. They may  
 CC also be used to study the expression and function of PDE-XIV  
 CC polypeptides and their role in metabolism. The PDE-XIV polypeptides  
 CC may be used as antigens in the production of antibodies against PDE-XIV  
 CC and in assays to identify modulators (agonists and antagonists) of  
 CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and  
 CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression  
 CC used in the preparation of a composition for the treatment of a disorder  
 CC associated with inappropriate PDE-XIV expression and/or activity and to  
 CC screen for agents that can modulate PDE-XIV expression and/or activity.  
 CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for  
 CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by  
 CC enzyme linked immunosorbant assay (ELISA)).  
 XX Sequence 437 AA;  
 SQ Query Match 100.0%; Score 61; DB 21; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 0.04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSLCIVERGE 11  
 DB 1 MSLCIVERGE 11  
 ID AAY93573 standard; Protein; 445 AA.  
 XX AAY93573;  
 AC AAY93573;  
 DT 25-SEP-2000 (first entry)  
 XX Amino acid sequence of a phosphodiesterase enzyme.  
 DE

XX Phosphodiesterase; PDE-XIV; enzyme.  
 KW Synthetic.  
 XX Location/Qualifiers  
 OS Key  
 FH MISC-difference 12 /label= Val, Ile  
 FT MISC-difference 16  
 FT MISC-difference 16 /label= Ser, Asn  
 FT MISC-difference 18 /label= Glu, Asp  
 FT MISC-difference 20..21 /label= Ser, Val, Asp, Ala  
 FT /note- "these residues are a peptide comprising at least two or more of the above residues"  
 FT MISC-difference 30 /label= Val, Ile  
 FT MISC-difference 39 /label= Pro, Arg  
 FT MISC-difference 56 /label= Asn, Ser  
 FT MISC-difference 59 /label= His, Tyr  
 FT MISC-difference 114 /label= Thr, Met  
 FT MISC-difference 141 /label= Ser, Thr  
 FT MISC-difference 168..169 /label= Gly, His, Ser, Gln  
 FT /note- "these residues are a peptide comprising at least two or more of the above residues"  
 FT MISC-difference 307..308 /label= Asp, Ala, Asn, Val  
 FT /note- "these residues are a peptide comprising at least two or more of the above residues"  
 FT MISC-difference 350 /label= Glu, Asp  
 FT MISC-difference 379 /label= Ser, Thr  
 FT MISC-difference 391 /label= His, Arg  
 FT MISC-difference 404 /label= Gly, Ser  
 FT MISC-difference 418..419 /label= Pro, Arg, Ser, Asn  
 FT /note- "these residues are a peptide comprising at least two or more of the above residues"  
 FT MISC-difference 423 /label= Ser, Arg  
 FT MISC-difference 427..428 /label= Ser, Gly, Pro, Asp, His, Gln  
 FT /note- "these residues are a peptide comprising at least two or more of the above residues"  
 FT MISC-difference 430 /label= His, Leu  
 FT MISC-difference 433..434 /label= Gln, Gly, Thr, Pro, Ala  
 FT /note- "these residues are a peptide comprising at least two or more of the above residues"  
 FT MISC-difference 436..437 /label= Ser, Glu, Thr, Leu  
 FT /note- "these residues are a peptide comprising at least two or more of the above residues"  
 FT MISC-difference 440 /note- "optionally absent"  
 FT MISC-difference 443..444 /label= Asp, Ser, Ala, Thr  
 FT /note- "these residues are a peptide comprising at least two or more of the above residues"  
 PN EPI1018559-A1.

```

XX 12-JUL-2000.
PD
XX
PF 09-NOV-1999; 99EP-0308902.
XX
PR 23-DEC-1998; 98GB-0028603.
PR 17-SEP-1999; 99GB-0022123.
XX
PA (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
PI Fldock M;
XX
DR WPI: 2000-433274/38.
XX
PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT useful for preventing diagnosing and treating diseases associated with
PT inappropriate PDE-XIV expression and/or activity -
XX
PS Disclosure; Page 64-66; 104pp; English.
XX
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.
CC The enzyme sequence is derived from a formula of the invention. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC may be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).
XX
SQ Sequence 445 AA;

```

```

Query Match 100.0%; Score 61; DB 21; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MSCIMVERGE 11
DB 1 MSCIMVERGE 11

```

```

RESULT 7
AA93567
ID AA93567 standard; Protein; 446 AA.
XX
XX AA93567;
AC
XX
XX 25-SEP-2000 (first entry)
DT
XX
XX Amino acid sequence of a murine phosphodiesterase enzyme.
DE
XX Phosphodiesterase; PDE-XIV; murine; enzyme.
KM
XX
XX Mus sp.
OS
XX EP1018559-A1.
PN
XX 12-JUL-2000.
PD
XX
XX 09-NOV-1999; 99EP-0308902.
XX

```

```

PR 23-DEC-1998; 98GB-0028603.
PR 17-SEP-1999; 99GB-0022123.
XX
XX (PFIZ ) PFIZER LTD.
PA (PFIZ ) PFIZER INC.
XX
XX Fldock M;
XX
DR WPI: 2000-433274/38.
DR N-PSDB: AAA46649.
XX
XX
XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
XX useful for preventing diagnosing and treating diseases associated with
XX inappropriate PDE-XIV expression and/or activity -
XX
PS Disclosure; Page 39-41; 104pp; English.
XX
CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC may be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).
XX
SQ Sequence 446 AA;

```

```

Query Match 100.0%; Score 61; DB 21; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MSCIMVERGE 11
DB 1 MSCIMVERGE 11

```

```

RESULT 8
AA93574
ID AA93574 standard; Protein; 446 AA.
XX
XX AA93574;
AC
XX
XX 25-SEP-2000 (first entry)
DT
XX
XX Amino acid sequence of a phosphodiesterase enzyme.
DE
XX Phosphodiesterase; PDE-XIV; enzyme.
KW
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 12 /label= Val, Ile
FT Misc-difference 16 /label= Ser, Asn
FT Misc-difference 18 /label= Glu, Asp
FT Misc-difference 20 /label= Ser, Val, Asn, Ala
FT Misc-difference 21 /label= Ser, Val, Asn, Ala
FT

```

FT	Misc-difference	30	/label= Val, Ile
FT	Misc-difference	39	/label= Pro, Arg
FT	Misc-difference	56	/label= Asn, Ser
FT	Misc-difference	59	/label= His, Tyr
FT	Misc-difference	114	/label= Thr, Met
FT	Misc-difference	141	/label= Ser, Thr
FT	Misc-difference	168	/label= Gly, His, Ser, Gln
FT	Misc-difference	169	/label= Gly, His, Ser, Gln
FT	Misc-difference	307	/label= Asp, Ala, Asn, Val
FT	Misc-difference	308	/label= Asp, Ala, Asn, Val
FT	Misc-difference	350	/label= Asp, Ala, Asn, Val
FT	Misc-difference	379	/label= Glu, Asp
FT	Misc-difference	391	/label= Ser, Thr
FT	Misc-difference	404	/label= His, Arg
FT	Misc-difference	418	/label= Gly, Ser
FT	Misc-difference	419	/label= Pro, Arg, Ser, Asn
FT	Misc-difference	423	/label= Pro, Arg, Ser, Asn
FT	Misc-difference	430	/label= Ser, Arg
FT	Misc-difference	433	/label= His, Leu
FT	Misc-difference	434	/label= Gln, Gly, Thr, Pro, Ala
FT	Misc-difference	435	/label= Gln, Gly, Thr, Pro, Ala
FT	Misc-difference	437	/label= Gln, Gly, Thr, Pro, Ala
FT	Misc-difference	438	/label= Ser, Glu, Thr, Leu
FT	Misc-difference	441	/label= Ser, Glu, Thr, Leu
FT	Misc-difference	444	/note= "optionally absent"
FT	Misc-difference	445	/label= Asp, Ser, Ala, Thr
XX	Misc-difference		/label= Asp, Ser, Ala, Thr
XX	EP1018559-A1.		
XX	12-JUL-2000.		
XX	09-NOV-1999;	99EP-0308902.	
XX	23-DEC-1998;	98GB-0028603.	
XX	17-SEP-1999;	99GB-0022123.	
XX	(PF12 ) PFIZER LTD.		
XX	(PF12 ) PFIZER INC.		
XX	PI		
XX	PIdock M;		
XX	WPI; 2000-433274/38.		
XX	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes		
XX	useful for preventing diagnosing and treating diseases associated with		
XX	inappropriate PDE-XIV expression and/or activity -		

The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).

Sequence 446 AA:

Query Match 100.0%; Score 61; DB 21; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 0.041;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLMERGE 11  
 1111111111  
 Db 1 MSCLMERGE 11

RESULT 9  
 AAY93569  
 ID AAY93569 standard; Protein; 450 AA.  
 XX  
 AC AAY93569;  
 XX  
 DT 25-SEP-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human phosphodiesterase enzyme.  
 XX  
 KW Phosphodiesterase; PDE-XIV; human; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1018559-A1.  
 XX  
 PD 12-JUL-2000.  
 XX  
 PF 09-NOV-1999; 99EP-0308902.  
 XX  
 PR 23-DEC-1998; 98GB-0028603.  
 XX  
 PR 17-SEP-1999; 99GB-0022123.  
 XX  
 PA (PF12 ) PFIZER LTD.  
 XX  
 PA (PF12 ) PFIZER INC.  
 XX  
 PI Fldock M;  
 XX  
 DR WPI: 2000-433274/38.  
 XX  
 DR N-PSDB: AAAA6651.  
 XX  
 PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,  
 XX  
 PT useful for preventing diagnosing and treating diseases associated with  
 XX  
 PT inappropriate PDE-XIV expression and/or activity -  
 XX  
 PS Disclosure: Page 45-47; 104pp; English.

CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PDE-XIV expression. For example, the polynucleotide  
CC be administered to treat diseases by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of PDE-XIV. They may  
CC also be used to study the expression and function of PDE-XIV  
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides  
CC may be used as antigens in the production of antibodies against PDE-XIV  
CC and in assays to identify modulators (agonists and antagonists) of  
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and  
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression  
CC and activity (i.e. the PDE-XIV gene and/or expression product may be  
CC used in the preparation of a composition for the treatment of a disorder  
CC associated with inappropriate PDE-XIV expression and/or activity and to  
CC screen for agents that can modulate PDE-XIV expression and or activity.  
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for  
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by  
CC enzyme linked immunosorbent assay (ELISA)).

SO Sequence 450 AA:

Query Match 100.0%; Score 61; DB 21; Length 450;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLWERCGE 11  
DB 1 MSCLWERCGE 11

RESULT 10

ID AAG78915  
AAG78915 standard; Protein; 450 AA.

AC AAG78915;

DT 19-DEC-2001 (first entry)

DE Human type 7B phosphodiesterase, PDE7B.

KM Human; type 7B phosphodiesterase; PDE7B; enzyme.

OS Homo sapiens.

PN JP2001238680-A.

PD 04-SEP-2001.

PF 03-MAR-2000; 2000JP-0058159.

PR 03-MAR-2000; 2000JP-0058159.

PA (TANA ) TANABE SEIYAKU CO.

DR WPI: 2001-610057/70.

N-PSDB; AAT70009.

PT New phosphodiesterase for use in the development of inhibitors of high  
selectivity and drugs of low side effect -  
PS Claim 2; Page 12-14; 18pp; Japanese.

CC The present sequence is the protein sequence for human type 7B  
CC phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the  
CC development of inhibitors of high selectivity and drugs of low side  
CC effects.

SO Sequence 450 AA:

Query Match 100.0%; Score 61; DB 22; Length 450;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLWERCGE 11

DB 1 MSCLWERCGE 11

RESULT 11

ID AAU08675  
AAU08675 standard; Protein; 450 AA.

AC AAU08675;

DT 18-DEC-2001 (first entry)

DE Human phosphodiesterase type 7B #1.

KM Human; phosphodiesterase type 7B; cardiovascular disease;  
KM asthma; allergy; inflammatory disease; immune-related disorder;  
KM cardiovascular; antiallergic; immunosuppressive;  
KM antiinflammatory.

OS Homo sapiens.

PN WO200162940-A2.

PD 30-AUG-2001.

PF 20-FEB-2001; 2001WO-EP01858.

PR 21-FEB-2000; 2000EP-0103655.

PA (MERE ) MERCK PATENT GMBH.

PI Kluxen F, Hentsch B;

DR WPI: 2001-570636/64.

N-PSDB; AAS13248.

PT Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,  
diagnosing and treating, e.g. asthma, inflammation and allergies -  
PS Claim 1; Page 36-37; 40pp; English.

CC The invention relates to a novel human phosphodiesterase type 7B  
CC polypeptide and the nucleic acid that encodes it. The protein and nucleic  
CC acid may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For  
CC example, The protein and nucleic acid may be used to treat  
CC disorders associated with decreased expression by rectifying mutations  
CC or deletions in a patient's genome that affect the activity of P7B by  
CC expressing inactive proteins or to supplement the patients own  
CC production of P7B. The nucleic acids may be used to produce P7B  
CC polypeptides, by inserting the nucleic acids into a host cell and  
CC culturing the cell to express the protein. The nucleic acid and its  
CC complements may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The P7B  
CC polypeptides may also be used as antigens in the production of  
CC antibodies against P7B and in assays to identify modulators of it's  
CC expression and activity. The anti-P7B antibodies and antagonists may  
CC also be used to down regulate expression and activity. The anti-P7B  
CC antibodies may also be used as diagnostic agents for detecting the  
CC presence of P7B in samples (e.g. by enzyme linked immunosorbent assay  
CC (ELISA)). Disorders that may be prevented, diagnosed and/or treated by  
CC the above methods include, for example cardiovascular disease, asthma,  
CC allergy, inflammation, and immune-related disorders. The present  
CC sequence represents a human phosphodiesterase 7B.

SO Sequence 450 AA:

Query Match 100.0%; Score 61; DB 22; Length 450;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLWERCGE 11

Db 1 MSCLMVERGCE 11

|||||

RESULT 12

AA93575

AA93575 standard; Protein; 451 AA.

AC AA93575;

DE 25-SEP-2000 (first entry)

DE Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; enzyme.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 12

FT /label- Val, Ile

FT Misc-difference 16

FT /label- Ser, Asn

FT Misc-difference 18

FT /label- Glu, Asp

FT Misc-difference 20

FT /label- Ser, Val, Asn, Ala

FT Misc-difference 21

FT /label- Ser, Val, Asn, Ala

FT Misc-difference 30

FT /label- Val, Ile

FT Misc-difference 39

FT /label- Pro, Arg

FT Misc-difference 56

FT /label- Asn, Ser

FT Misc-difference 59

FT /label- His, Tyr

FT Misc-difference 114

FT /label- Thr, Met

FT Misc-difference 141

FT /label- Ser, Thr

FT Misc-difference 168

FT /label- Gly, His, Ser, Gln

FT Misc-difference 169

FT /label- Gly, His, Ser, Gln

FT Misc-difference 307

FT /label- Asp, Ala, Asn, Val

FT Misc-difference 308

FT /label- Asp, Ala, Asn, Val

FT Misc-difference 350

FT /label- Glu, Asp

FT Misc-difference 379

FT /label- Ser, Thr

FT Misc-difference 391

FT /label- His, Arg

FT Misc-difference 404

FT /label- Gly, Ser

FT Misc-difference 418

FT /label- Pro, Arg, Ser, Asn

FT Misc-difference 419

FT /label- Pro, Arg, Ser, Asn

FT Misc-difference 423

FT /label- Ser, Arg

FT Misc-difference 435

FT /label- His, Leu

FT Misc-difference 438..440

FT /note- "these residues are either Gln-Gly-Pro or Pro-Ala-Pro"

FT Misc-difference 442..443

FT /note- "these residues are either Ser-Glu or Thr-Leu"

FT Misc-difference 446

FT /note- "optionally absent"

FT Misc-difference 449..450

FT /note- "these residues are either Asp-Ser or Ala-Thr"

FT EPI018559-A1.

PD 12-JUL-2000.

XX

XX

XX

XX

XX 09-NOV-1999; 99EP-0308902.

XX

XX 23-DEC-1998; 98GB-0028603.

XX 17-SEP-1999; 99GB-0022123.

XX

XX (PRTZ ) PRIZER LTD.

XX (PRTZ ) PRIZER INC.

XX

XX Fldock M:

XX

XX WPI: 2000-433274/38.

XX

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity -

XX Disclosure; Page 75-78; 104pp; English.

XX

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA)).

XX

XX Sequence 451 AA;

XX

XX Query Match 100.0%; Score 61; DB 21; Length 451;

XX Best Local Similarity 100.0%; Pred. NO. 0.041;

XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSCLMVERGCE 11

Db 1 MSCLMVERGCE 11

AA93575

AA93575 standard; protein; 19 AA.

AC AA93575;

DE 25-SEP-2001 (first entry)

XX

XX Human secreted protein encoded by gene No. 75 (clone id HB8TY90).

XX

XX Secreted protein; immunosuppressive; antiarthritic; antiinflammatory; antiproliferative; cytostatic; cardiact; vasotrophic; cerebroprotective; neuroprotective; antibacterial; virucide; fungicide; human; opthalmological; gene therapy.

XX

OS Homo sapiens.  
XX  
XX MO200155430-A1.  
XX  
XX  
PD 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01431.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 12-SEP-2000; 2000US-0231968.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
PI Moore PA, Wei P, Edner R, Duan DR, Shi T, Choi GH, Fiscella M;  
PI Ni J, Ruben SM, Barash SC;  
XX  
XX WPI; 2001-476220/51.  
XX  
XX 17 isolated nucleic acid molecules encoding human secreted proteins,  
PT used to preventing, treating or ameliorating a medical condition  
XX  
XX Disclosure; Page 19; 482pp; English.  
XX  
XX The invention provides novel human secreted proteins and polynucleotides  
CC encoding them. The secreted proteins can be expressed by standard  
CC recombinant methodology. The secreted proteins and polynucleotides are  
CC used to prevent, treat or ameliorate a medical condition in e.g. humans,  
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can  
CC also be used in diagnosing a pathological condition. The antibodies to  
CC the proteins can also be used in alleviating symptoms associated with the  
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme  
CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or  
CC treated include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
CC ocular disorders e.g. corneal infection. The polypeptides can also be  
CC used to aid wound healing and epithelial cell proliferation, to prevent  
CC skin aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis. The polypeptides can also be used as a food additive or  
CC preservative to increase or decrease storage capabilities. The present  
CC sequence represents a human secreted protein.  
XX  
XX Sequence 19 AA;  
SQ  
Query Match 67.2%; Score 41; DB 22; Length 19;  
Best Local Similarity 75.0%; Pred. No. 3.8;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 3 CLIMVERCG 10  
Db 3 CLIMVERCG 10  
||:|:|:|  
|:|:|:|  
RESULT 14  
AAB85565  
ID AAB85565 standard; protein; 23 AA.  
XX  
XX AAB85565;  
AC  
XX  
XX 25-SEP-2001 (first entry)  
DT  
XX  
XX Human secreted protein encoded by gene No.75 (clone Id HB8TY90).  
DE  
XX  
XX Secreted protein; immunosuppressive; antiarthritic; antipneumatic;  
KW antiproliferative; cytoskeletal; cardiatic; vasotropic; cerebroprotective;  
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; human;  
KW ophthalmological; gene therapy.  
XX

OS Homo sapiens.  
XX  
XX MO200155430-A1.  
XX  
XX  
PD 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01431.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 12-SEP-2000; 2000US-0231968.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
PI Moore PA, Wei P, Edner R, Duan DR, Shi T, Choi GH, Fiscella M;  
PI Ni J, Ruben SM, Barash SC;  
XX  
XX WPI; 2001-476220/51.  
XX  
XX 17 isolated nucleic acid molecules encoding human secreted proteins,  
PT used to preventing, treating or ameliorating a medical condition  
XX  
XX Disclosure; Page 19; 482pp; English.  
XX  
XX The invention provides novel human secreted proteins and polynucleotides  
CC encoding them. The secreted proteins can be expressed by standard  
CC recombinant methodology. The secreted proteins and polynucleotides are  
CC used to prevent, treat or ameliorate a medical condition in e.g. humans,  
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can  
CC also be used in diagnosing a pathological condition. The antibodies to  
CC the proteins can also be used in alleviating symptoms associated with the  
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme  
CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or  
CC treated include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
CC ocular disorders e.g. corneal infection. The polypeptides can also be  
CC used to aid wound healing and epithelial cell proliferation, to prevent  
CC skin aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis. The polypeptides can also be used as a food additive or  
CC preservative to increase or decrease storage capabilities. The present  
CC sequence represents a human secreted protein.  
XX  
XX Sequence 23 AA;  
SQ  
Query Match 67.2%; Score 41; DB 22; Length 23;  
Best Local Similarity 75.0%; Pred. No. 4.5;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 3 CLIMVERCG 10  
Db 1 CLIMVERCG 8  
||:|:|:|  
|:|:|:|  
RESULT 15  
AAB85564  
ID AAB85564 standard; protein; 47 AA.  
XX  
XX AAB85564;  
AC  
XX  
XX 25-SEP-2001 (first entry)  
DT  
XX  
XX Human secreted protein encoded by gene No.75 (clone Id HB8TY90).  
DE  
XX  
XX Secreted protein; immunosuppressive; antiarthritic; antipneumatic;  
KW antiproliferative; cytoskeletal; cardiatic; vasotropic; cerebroprotective;  
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; human;  
KW ophthalmological; gene therapy.  
XX

OS Homo sapiens.  
 XX WO20015430-A1.  
 PN 02-AUG-2001.  
 XX  
 PD 17-JAN-2001; 2001WO-US01431.  
 XX  
 PF 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 12-SEP-2000; 2000US-0231968.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
 PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;  
 PI Ni J, Ruben SM, Barash SC;  
 XX  
 DR WPI; 2001-476220/51.  
 XX  
 XX 17 isolated nucleic acid molecules encoding human secreted proteins,  
 PT used to preventing, treating or ameliorating a medical condition -  
 PS Disclosure; Page 19; 482pp; English.  
 XX  
 CC The invention provides novel human secreted proteins and polynucleotides  
 CC encoding them. The secreted proteins can be expressed by standard  
 CC recombinant methodology. The secreted proteins and polynucleotides are  
 CC used to prevent, treat or ameliorate a medical condition in e.g. humans,  
 CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can  
 CC also be used in diagnosing a pathological condition. The antibodies to  
 CC the proteins can also be used in alleviating symptoms associated with the  
 CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme  
 CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or  
 CC treated include autoimmune diseases e.g. rheumatoid arthritis,  
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
 CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.  
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
 CC ocular disorders e.g. corneal infection. The polypeptides can also be  
 CC used to aid wound healing and epithelial cell proliferation, to prevent  
 CC skin aging due to sunburn, to maintain organs before transplantation, for  
 CC supporting cell culture of primary tissues, to regenerate tissues and in  
 CC chemotaxis. The polypeptides can also be used as a food additive or  
 CC preservative to increase or decrease storage capabilities. The present  
 CC sequence represents a human secreted protein.  
 XX  
 SQ Sequence 47 AA:  
 Query Match: 67.2%; Score 41; DB 22; Length 47;  
 Best Local Similarity 75.0%; Pred. No. 8.6;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 CLAMVRCG 10  
 11:1:111  
 DB 25 CLLVORCG 32

Search completed: October 27, 2002, 09:21:13  
 Job time : 63 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 27, 2002, 09:20:16 ; Search time 25 Seconds  
(without alignments)  
10.747 Million cell updates/sec

Title: US-09-471-459A-9  
Perfect score: 61  
Sequence: 1 MSLMVERGE 11

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	39	63.9	102	1	US-08-469-427A-2	Sequence 2, Appli
2	39	63.9	102	2	US-08-609-443B-2	Sequence 2, Appli
3	39	63.9	102	2	US-08-569-063C-2	Sequence 2, Appli
4	39	63.9	133	1	US-08-469-427A-9	Sequence 9, Appli
5	39	63.9	133	2	US-08-609-443B-9	Sequence 9, Appli
6	39	63.9	133	2	US-08-569-063C-9	Sequence 9, Appli
7	39	63.9	188	1	US-08-469-427A-5	Sequence 5, Appli
8	39	63.9	188	1	US-08-469-427A-11	Sequence 11, Appli
9	39	63.9	188	2	US-08-609-443B-5	Sequence 5, Appli
10	39	63.9	188	2	US-08-609-443B-11	Sequence 11, Appli
11	39	63.9	188	2	US-08-569-063C-5	Sequence 5, Appli
12	39	63.9	188	2	US-08-569-063C-11	Sequence 11, Appli
13	39	63.9	188	4	US-08-795-430-57	Sequence 57, Appli
14	39	63.9	195	1	US-08-469-427A-7	Sequence 7, Appli
15	39	63.9	195	2	US-08-609-443B-7	Sequence 7, Appli
16	39	63.9	195	2	US-08-569-063C-7	Sequence 7, Appli
17	39	63.9	207	2	US-08-609-443B-13	Sequence 13, Appli
18	39	63.9	207	2	US-08-609-443B-15	Sequence 15, Appli
19	39	63.9	207	2	US-08-569-063C-13	Sequence 13, Appli
20	39	63.9	207	2	US-08-569-063C-15	Sequence 15, Appli
21	36	59.0	254	4	US-09-449-437A-4	Sequence 4, Appli
22	36	59.0	254	4	US-09-449-437A-6	Sequence 6, Appli
23	35	57.4	787	1	US-08-574-763-2	Sequence 2, Appli
24	34	55.7	20	4	US-08-817-895-12	Sequence 12, Appli
25	34	55.7	164	1	US-07-970-462A-2	Sequence 2, Appli
26	34	55.7	164	1	US-08-154-915-6	Sequence 6, Appli
27	34	55.7	164	1	US-08-275-983B-4	Sequence 4, Appli

# ALIGNMENTS

28	34	55.7	164	1	US-08-406-248-2	Sequence 2, Appli
29	34	55.7	164	1	US-08-574-043A-2	Sequence 2, Appli
30	34	55.7	164	2	US-08-524-218A-2	Sequence 2, Appli
31	34	55.7	164	2	US-08-795-015-2	Sequence 2, Appli
32	34	55.7	164	4	US-08-456-297-2	Sequence 2, Appli
33	34	55.7	164	4	US-08-794-002-23	Sequence 23, Appli
34	34	55.7	164	4	US-08-854-039B-24	Sequence 24, Appli
35	34	55.7	164	5	PCT-US92-10904-2	Sequence 2, Appli
36	34	55.7	164	5	PCT-US94-09700-2	Sequence 2, Appli
37	34	55.7	164	5	PCT-US94-12936-2	Sequence 2, Appli
38	34	55.7	164	5	PCT-US96-11886A-2	Sequence 2, Appli
39	34	55.7	397	5	PCT-US94-09700-11	Sequence 11, Appli
40	34	54.1	95	3	US-08-970-403-2	Sequence 2, Appli
41	33	54.1	96	1	US-08-347-492B-4	Sequence 4, Appli
42	33	54.1	96	2	US-08-798-143-4	Sequence 2, Appli
43	33	54.1	96	2	US-08-458-355A-2	Sequence 2, Appli
44	33	54.1	96	4	US-08-613-822-2	Sequence 2, Appli
45	33	54.1	96	5	PCT-US95-15484-4	Sequence 4, Appli

RESULT 1  
US-08-469-427A-2  
Sequence 2, Application US/08469427A  
Patent No. 5607918  
GENERAL INFORMATION:  
APPLICANT: Eriksson, Ulf  
APPLICANT: Olofsson, Birgitta  
APPLICANT: Alitalo, Katri  
APPLICANT: Pajusola, Katri  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Evenson, McKee, Edwards & Lenahan  
STREET: 1200 G Street, N.W., Suite 700  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,427A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/397,651  
FILING DATE: 01-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 41979cp2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 102 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE: mouse embryo  
TISSUE TYPE:  
US-08-469-427A-2

Query Match 63.9%; Score 39; DB 1; Length 102;

Best Local Similarity 66.7%; Pred. No. 6;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERCG 10  
||:|:|:|  
Db 40 SCVTVORCG 48

RESULT 2  
US-08-609-443B-2  
; Sequence 2, Application US/08609443B  
; Patent No. 5840693  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ALITALO, Kari  
; APPLICANT: PAJUSOLA, Kari  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
; TITLE OF INVENTION: DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKown, Edwards & Lenahan, P.L.L.C.  
; STREET: 1200 G Street, N.W., Suite 700  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/609,443B  
; FILING DATE: 01-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/397,651  
; FILING DATE: 01-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/469,427  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/569,063  
; FILING DATE: 06-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EVANS, Joseph D  
; REGISTRATION NUMBER: 26,269  
; REFERENCE/DOCKET NUMBER: 1064/41979CP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-8800  
; TELEFAX: (202) 628-8844  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 102 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; TISSUE TYPE: mouse embryo  
US-08-609-443B-2

Query Match 63.9%; Score 39; DB 2; Length 102;  
Best Local Similarity 66.7%; Pred. No. 6;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERCG 10  
||:|:|:|  
Db 40 SCVTVORCG 48

RESULT 3  
US-08-569-063C-2  
; Sequence 2, Application US/08569063C  
; Patent No. 5928939  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ALITALO, Kari  
; APPLICANT: PAJUSOLA, Kari  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
; TITLE OF INVENTION: DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKown, Edwards & Lenahan, P.L.L.C.  
; STREET: 1200 G Street, N.W., Suite 700  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/569,063C  
; FILING DATE: 06-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/469,427  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/397,651  
; FILING DATE: 01-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EVANS, Joseph D  
; REGISTRATION NUMBER: 26,269  
; REFERENCE/DOCKET NUMBER: 1064/41979CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-8800  
; TELEFAX: (202) 628-8844  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 102 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; TISSUE TYPE: mouse embryo  
US-08-569-063C-2

Query Match 63.9%; Score 39; DB 2; Length 102;  
Best Local Similarity 66.7%; Pred. No. 6;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERCG 10  
||:|:|:|  
Db 40 SCVTVORCG 48

RESULT 4  
US-08-469-427A-9  
; Sequence 9, Application US/08469427A  
; Patent No. 5607918  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ALITALO, Kari  
; APPLICANT: PAJUSOLA, Kari  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
; TITLE OF INVENTION: DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
; STREET: 1200 G Street, N.W., Suite 700  
; CITY: Washington  
; STATE: DC  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,427A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/397,651  
; FILING DATE: 01-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Evans, Joseph D  
; REGISTRATION NUMBER: 26,269  
; REFERENCE/DOCKET NUMBER: 41979CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-8800  
; TELEFAX: (202) 628-8844  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 133 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-469-427A-9

Query Match 63.9%; Score 39; DB 1; Length 133;  
Best Local Similarity 66.7%; Pred. No. 7.7;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLMVERCG 10  
II: I:III  
Db 71 SCVTWORCG 79

RESULT 5  
US-08-609-443B-9  
; Sequence 9, Application US/08609443B  
; Patent No. 5840693  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ALITALO, Kari  
; APPLICANT: PAJUSOLA, Katri  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
; TITLE OF INVENTION: DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.  
; STREET: 1200 G Street, N.W., Suite 700  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/609,443B  
; FILING DATE: 01-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/397,651

; FILING DATE: 01-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/469,427  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/569,063  
; FILING DATE: 06-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EVANS, Joseph D  
; REGISTRATION NUMBER: 26,269  
; REFERENCE/DOCKET NUMBER: 1064/41979CP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-8800  
; TELEFAX: (202) 628-8844  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 133 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-609-443B-9

Query Match 63.9%; Score 39; DB 2; Length 133;  
Best Local Similarity 66.7%; Pred. No. 7.7;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLMVERCG 10  
II: I:III  
Db 71 SCVTWORCG 79

RESULT 6  
US-08-569-063C-9  
; Sequence 9, Application US/08569063C  
; Patent No. 5928939  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: OLOFSSON, Birgitta  
; APPLICANT: ALITALO, Kari  
; APPLICANT: PAJUSOLA, Katri  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
; TITLE OF INVENTION: DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.  
; STREET: 1200 G Street, N.W., Suite 700  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/569,063C  
; FILING DATE: 06-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/469,427  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/397,651  
; FILING DATE: 01-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EVANS, Joseph D  
; REGISTRATION NUMBER: 26,269  
; REFERENCE/DOCKET NUMBER: 1064/41979CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-8800  
; TELEFAX: (202) 628-8844  
; INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-063C-9

Query Match 63.9%; Score 39; DB 2; Length 133;  
Best Local Similarity 66.7%; Pred. No. 7.7;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERG 10  
11: 1:111  
Db 71 SCVTVORCG 79

## RESULT 7

US-08-469-427A-5  
Sequence 5, Application US/08469427A  
Patent No. 5607918

GENERAL INFORMATION:  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: Olofsson, Birgitta  
APPLICANT: Alitalo, Kari  
APPLICANT: Pajusola, Katri  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
STREET: 1200 G Street, N.W., Suite 700  
CITY: Washington  
STATE: DC  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,427A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/397,651  
FILING DATE: 01-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 41979CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
TISSUE TYPE: adult mouse heart  
US-08-469-427A-5

Query Match 63.9%; Score 39; DB 1; Length 188;  
Best Local Similarity 66.7%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERG 10  
11: 1:111  
Db 71 SCVTVORCG 79

RESULT 8  
US-08-469-427A-11  
Sequence 11, Application US/08469427A  
Patent No. 5607918

GENERAL INFORMATION:  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: Olofsson, Birgitta  
APPLICANT: Alitalo, Kari  
APPLICANT: Pajusola, Katri  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
STREET: 1200 G Street, N.W., Suite 700  
CITY: Washington  
STATE: DC  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,427A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/397,651  
FILING DATE: 01-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 41979CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
TISSUE TYPE: human fibrosarcoma  
US-08-469-427A-11

Query Match 63.9%; Score 39; DB 1; Length 188;  
Best Local Similarity 66.7%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERG 10  
11: 1:111  
Db 71 SCVTVORCG 79

## RESULT 9

US-08-609-443B-5  
Sequence 5, Application US/08609443B  
Patent No. 5840693

GENERAL INFORMATION:  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: Olofsson, Birgitta  
APPLICANT: Alitalo, Kari  
APPLICANT: Pajusola, Katri  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-609-443B-5

Query Match          63.9%; Score 39; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 SCLWVRG 10
      11: 11111
Db      71 SCVTYGRG 79

RESULT 10
US-08-609-443B-11
; Sequence 11, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Karl
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: human fibrosarcoma
; US-08-609-443B-11

Query Match          63.9%; Score 39; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 SCLWVRG 10
      11: 11111
Db      71 SCVTYGRG 79

RESULT 11
US-08-569-063C-5
; Sequence 5, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Karl
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427

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Mon Oct 28 10:52:00 2002

us-09-471-459a-9\_1.rai

Page 6

FILED DATE: 06-JUN-1995  
PRIOR APPLICATION DATA: US 08/397,651  
APPLICATION NUMBER: US 08/397,651  
FILING DATE: 01-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: EVANS, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 1064/41979CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8844  
TELEFAX: (202) 628-8800  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
TISSUE TYPE: adult mouse heart  
US-08-569-063C-5

Query Match 63.9%; Score 39; DB 2; Length 188;  
Best Local Similarity 66.7%; Pred No. 11;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLMVERG 10  
11: 1:111  
DB 71 SCVTYORCG 79

RESULT 12  
US-08-569-063C-11  
Sequence 11, Application US/08569063C  
Patent No. 5928939  
GENERAL INFORMATION:  
APPLICANT: ERIKSSON, Ulf  
APPLICANT: OLOFSSON, Birgitta  
APPLICANT: ALITALO, Karl  
APPLICANT: PAJUSOLA, Kari  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
TITLE OF INVENTION: DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Evenson, McKee, Edwards & Lenahan, P.L.L.C.  
STREET: 1200 G Street, N.W., Suite 700  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,063C  
FILING DATE: 06-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/469,427  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/397,651  
FILING DATE: 01-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: EVANS, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 1064/41979CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
TISSUE TYPE: human fibrosarcoma  
US-08-569-063C-11

Query Match 63.9%; Score 39; DB 2; Length 188;  
Best Local Similarity 66.7%; Pred No. 11;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLMVERG 10  
11: 1:111  
DB 71 SCVTYORCG 79

RESULT 13  
US-08-795-430-57  
Sequence 57, Application US/08795430  
Patent No. 6130071  
GENERAL INFORMATION:  
APPLICANT: Joukov, Vladimir  
APPLICANT: Alitalo, Karl  
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,430  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI96/00427  
FILING DATE: 01-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/671,573  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/340,011  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GASS, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/33691  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 57:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-430-57

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Query Match          63.9%; Score 39; DB 4; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      2 SCLMVERCG 10
      11:1:111
Db      71 SCVTVORCG 79

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RESULT 14
US-08-469-427A-7
; Sequence 7, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Aitalo, Kari
; APPLICANT: Pajusola, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIORITY INFORMATION:
; APPLICATION DATA:
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 41979CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
US-08-469-427A-7

```

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Query Match          63.9%; Score 39; DB 1; Length 195;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      2 SCLMVERCG 10
      11:1:111
Db      71 SCVTVORCG 79

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RESULT 15
US-08-609-443B-7
; Sequence 7, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: AITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIORITY INFORMATION:
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
US-08-609-443B-7

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Query Match          63.9%; Score 39; DB 2; Length 195;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      2 SCLMVERCG 10
      11:1:111
Db      71 SCVTVORCG 79

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Search completed: October 27, 2002, 09:25:22  
Job time : 26 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2002, 07:31:22 ; Search time 25 Seconds

(without alignments)  
17.037 Million cell updates/sec

Title: US-09-471-459A-9

Perfect score: 61

Sequence: 1 MSCLMERCE 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	446	1	CN7B_MOUSE
2	61	100.0	450	1	CN7B_MOUSE
3	39	63.9	135	1	VEGB_RAT
4	39	63.9	207	1	VEGB_BOVIN
5	39	63.9	207	1	VEGB_HUMAN
6	39	63.9	207	1	VEGB_MOUSE
7	37	60.7	208	1	CRP2_HUMAN
8	36	59.0	273	1	SZ16_HUMAN
9	35	57.4	124	1	NUDM_HUMAN
10	35	57.4	477	1	U4F9_HSVJ
11	35	57.4	765	1	ECR2_HUMAN
12	35	57.4	787	1	ECR2_BOVIN
13	35	57.4	1515	1	GLTB_AZOB
14	35	57.4	2144	1	GLT1_YEAST
15	34	55.7	76	1	CRP1_HUMAN
16	34	55.7	76	1	CRP1_MOUSE
17	34	55.7	163	1	TRIG2_HUMAN
18	34	55.7	164	1	CDN1_HUMAN
19	34	55.7	171	1	SBP2_ANTYA
20	34	55.7	303	1	U124_HSVSA
21	34	55.7	356	1	Y4ZB_RHISN
22	34	55.7	448	1	Y4QG_RHISN
23	34	55.7	477	1	UAP1_YEAST
24	34	55.7	496	1	G11L_HUMAN
25	34	55.7	515	1	DRTS_CRIFA
26	34	55.7	592	1	SYD_BACSU
27	34	55.7	3054	1	POLG_TEV
28	33	54.1	96	1	SYZ0_HUMAN
29	33	54.1	183	1	KITH_TOMPV
30	33	54.1	277	1	MOVP_TAV
31	33	54.1	324	1	CHI2_PEA
32	33	54.1	353	1	PROB_THEMA
33	33	54.1	395	1	YG15_YEAST

34	33	54.1	401	1	NADM_YEAST	006178 saccharomyc
35	33	54.1	512	1	YMO9_MYCTU	010398 mycobacteri
36	33	54.1	837	1	NCR2_HUMAN	015394 homo sapien
37	33	54.1	837	1	NCR2_MOUSE	035136 mus musculu
38	33	54.1	1089	1	UBP6_HUMAN	P35125 homo sapien
39	32.5	53.3	649	1	SCAG_HUMAN	P51170 homo sapien
40	32.5	53.3	650	1	SCAG_RAT	P37091 rattus norv
41	32.5	53.3	653	1	SCAG_MOUSE	026738 oryctolagus
42	32.5	53.3	655	1	SCAG_MOUSE	09w039 mus musculu
43	32	52.5	264	1	RP0D_SULAC	P39471 sulfolobus
44	32	52.5	279	1	YA22_METTH	027101 methanobact
45	32	52.5	294	1	TYSY_ENCCU	062584 encephalito

## ALIGNMENTS

```

RESULT 1
CN7B_MOUSE
ID CN7B_MOUSE STANDARD: PRT: 446 AA.
AC Q9QXQ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN PDE7B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20087273; PubMed-10618442;
RA Helman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
RT "Cloning and characterization of PDE7B, a CAMP-specific
RT phosphodiesterase."
RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J;
RX MEDLINE-20329226; PubMed-10872825;
RA Gardner C.E., Robas N.M., Cawkill D., Flidock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
RT CAMP-specific nucleotide phosphodiesterase."
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC ADENOSINE 5'-PHOSPHATE.
CC -1- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
CC -1- ENZYME REGULATION: INHIBITED BY DIPHENYLMOLE, IBMX AND SCH51866.
CC -1- INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MILRINONE.
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF190639; AAF25195.1; -.
DR EMBL: A0251859; CAB92530.1; -.
DR MGD: MGI:1352752; Pde7b.
DR InterPro: IPR003607; HDC.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF00233; PDEase; 1.

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DR PRINTS: PR00387, PDIESTERASE1.  
DR SMART: SM00471; HDC: 1.  
DR PROSITE: PS00126; PDEASE\_1; 1.  
KW Hydrolase; CAMP.  
FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).  
SQ SEQUENCE 446 AA; 51337 MW; 7C052664B693A5AB CRC64;

Query Match 100.0%; Score 61; DB 1; Length 446;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLMERGE 11  
Db 1 MSCLMERGE 11

## RESULT 2

CN7B\_HUMAN STANDARD; PRT; 450 AA.  
AC O9NP56.  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).  
GN PDE7B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Brain;  
RX MEDLINE=20275458; PubMed=10814504;  
RA Sasaki T., Kotera J., Yuasa K., Omori K.;  
RT "Identification of human PDE7B, a CAMP-specific phosphodiesterase.";  
RL Biochem. Biophys. Res. Commun. 271:575-583(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Fetal brain;  
RX MEDLINE=20329226; PubMed=10872825;  
RA Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;  
RT "Cloning and characterisation of the human and mouse PDE7B, a novel  
Biochem. Biophys. Res. Commun. 272:186-192(2000).  
RL  
CC -1- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL  
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.  
CC -1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =  
CC ADENOSINE 5'-PHOSPHATE.  
CC -1- COFACTOR: REQUIRES Divalent CATIONS (BY SIMILARITY).  
CC -1- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.  
CC -1- INSENSITIVE TO ZAPRINAST, ROLIPRAM, AND MIRLONONE.  
CC -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN. ALSO EXPRESSED IN  
CC HEART, LIVER, SKELETAL MUSCLE AND PANCREAS.  
CC -1- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO  
CC PUTATIVE Divalent METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
CC FAMILY.  
CC  
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CC  
CC EMBL: AB038040; BAA96537.1; -;  
CC EMBL: AJ251860; CAB92441.1; -;  
CC MIM: 604645; -;  
CC InterPro: IPR003607; HDC.  
CC InterPro: IPR002073; PDEase.  
CC Pfam: PF00233; PDEase; 1.

DR PRINTS: PR00387, PDIESTERASE1.  
DR SMART: SM00471; HDC: 1.  
DR PROSITE: PS00126; PDEASE\_1; 1.  
KW Hydrolase; CAMP.  
FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).  
SQ SEQUENCE 450 AA; 51835 MW; EC142BF3E28D0028 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 450;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLMERGE 11  
Db 1 MSCLMERGE 11

## RESULT 3

VEGF\_RAT STANDARD; PRT; 135 AA.  
AC O33485; O54881;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Vascular endothelial growth factor B (VEGF-B) (VEGF related factor)  
DE (VRF) (Fragment).  
GN VEGFB OR VRF.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID:10116;  
RN [1]  
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM VEGF-B186).  
RC STRAIN-Sprague-Dawley; TISSUE-Placenta;  
RA Mandiote S.J., Pepper M.S.;  
RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM VEGF-B167).  
RC TISSUE-Heart;  
RA Well J., Eschenhagen T., Miltmann C., Scholz H.;  
RT Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds  
CC heparin and neuropilin-1 whereas the binding to neuropilin-1 of  
CC VEGF-B186 is regulated by proteolysis (By similarity).  
CC -1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer  
CC with vegf (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or  
CC to the extracellular matrix unless released by heparin (By  
CC similarity).  
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; VEGF-B186 (shown here)  
CC and VEGF-B167; are produced by alternative splicing.  
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
CC  
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CC  
CC EMBL: AF032925; AAB86884.1; -;  
CC EMBL: AF022952; AAB95447.1; -;  
CC HSSP: P15692; IYRP.  
CC InterPro: IPR000072; PDGF.  
CC Pfam: PF001629; PDGF; 1.  
CC ProDom: PD001629; PDGF; 1.  
CC SMART: SM00141; PDGF; 1.  
CC PROSITE: PS00249; PDGF\_1; 1.  
CC PROSITE: PS50278; PDGF\_2; 1.  
CC MitoGen; growth factor; Heparin-binding; Alternative splicing;  
CC Multigene family.  
CC NON\_TER 1 1  
FT DISULFID 47 91 BY SIMILARITY.

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FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 41 41 INTERCHAIN (BY SIMILARITY).
FT DISULFID 50 50 INTERCHAIN (BY SIMILARITY).
FT VARSPLIC 106 >135 RVALPHARPRSVLSWMSGASSPAII -> SPRTLCPC
      RCTPRVRPRDPTCRRCRCRRRFLHCGRGLNLPDTC
      (IN ISOFORM VEGF-B167).
FT CONFLICT 29 29 L -> F (IN REF. 2).
FT CONFLICT 37 37 L -> F (IN REF. 2).
FT CONFLICT 98 98 R -> K (IN REF. 2).
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15001 MW; A915863D8586F82D CRC64;

Query Match 63.9%; Score 39; DB 1; Length 135;
Best Local Similarity 66.7%; Pred. No. 3.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLWERCRCG 10
   11:11111
DB 40 SCVTQVRGCG 48

RESULT 4
VEGF_BOVIN STANDARD: PRT: 207 AA.
AC Q9XS49; Q9XS48; Q9GLX2;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor B precursor (VEGF-B) (VEGF related factor) (VRF).
GN VEGFB OR VRF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Liu X., Yonekura H., Yamagishi S., Yamamoto Y., Yamamoto H.;
RT "Structure and expression of bovine VEGF family.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 38-104 FROM N.A.
RC TISSUE=Heart;
RA Mandriota S.J., Pepper M.S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds
CC heparin and neuropilin-1 whereas the binding to neuropilin-1 of
CC VEGF-B166 is regulated by proteolysis (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer
CC with vegf (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; VEGF-B186 (shown here)
CC and VEGF-B167; are produced by alternative splicing.
CC -1- PTM: VEGF-B186 is O-glycosylated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
DR EMBL; AB004274; BAA77686.1; -
DR EMBL; AB004273; BAA77685.1; -
DR EMBL; AF099134; AAC29746.1; -
DR HSSP; P15692; IVPF.
DR InterPro; IPR000072; PDGF.

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DR Pfam; PF00341; PDGF. 1.
DR PRODOM; PD001629; PDGF. 1.
DR SMART; SM00141; PDGF. 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal; Heparin-binding;
KW Alternative splicing; Multigene family.
FT SIGNAL 1 21
FT CHAIN 22 207 POTENTIAL.
FT DISULFID 47 89 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
FT DISULFID 78 122 BY SIMILARITY.
FT DISULFID 82 124 BY SIMILARITY.
FT DISULFID 72 72 INTERCHAIN (BY SIMILARITY).
FT DISULFID 81 81 INTERCHAIN (BY SIMILARITY).
FT VARSPLIC 137 188 RASTPHRRPSPVPGWPGAGSPAIITPTPAPPSAH
      AAPSAALTP -> SPRLCPRCRPRDPTCRRCR
      RRSFLRCGRGLELNPDCRCRKLRR (IN ISOFORM
      VEGF-B167).
SQ SEQUENCE 207 AA; 21655 MW; 646C82DA1BE17782 CRC64;

Query Match 63.9%; Score 39; DB 1; Length 207;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLWERCRCG 10
   11:11111
DB 71 SCVTQVRGCG 79

RESULT 5
VEGF_HUMAN STANDARD: PRT: 207 AA.
AC P49765; Q16528;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor B precursor (VEGF-B) (VEGF related factor) (VRF).
GN VEGFB OR VRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS VEGF-B186 AND VEGF-B167).
RC TISSUE=Fetal brain;
RA MEDLINE=97077124; PubMed=8919691;
RA Pollock P., Lagercrantz J., Drinkwater C., Silins G., Thomson S.,
RA Hayward N.K., Weber G.;
RT "Cloning and characterization of a novel human gene related to
RT vascular endothelial growth factor.";
RL Genome Res. 6:124-131(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-B186).
RC TISSUE=Fibrosarcoma;
RA MEDLINE=96325041; PubMed=8702615;
RA Olofsson B., Pajusola K., von Euler G., Chillov D., Alltalo K.,
RA Eriksson U.;
RT "Genomic organization of the mouse and human genes for vascular
RT endothelial growth factor B (VEGF-B) and characterization of a second
RT splice isoform.";
RL J. Biol. Chem. 271:19310-19317(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-B167).
RX MEDLINE=96197355; PubMed=8637916;
RA Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA Saksela O., Orpana A., Pettersson R.F., Alltalo K., Eriksson U.;
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [4]

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RP SEQUENCE FROM N.A. (ISOFORM VEGF-B186).
RC TISSUE=Tonsil;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds
CC heparin and neuropilin-1 whereas the binding to neuropilin-1 of
CC VEGF-B186 is regulated by proteolysis.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer
CC with vegf.
CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin.
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms: VEGF-B186 (shown here)
CC and VEGF-B167; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Expressed in all tissues except liver. Highest
CC levels found in heart, skeletal muscle and pancreas.
CC -1- PTM: VEGF-B186 is O-glycosylated (by similarity).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
DR EMBL: U43368; AAA91462.1; -
DR EMBL: U43369; AAA91463.1; -
DR EMBL: U52819; AAC50721.1; -
DR EMBL: U48801; AAB06274.1; -
DR EMBL: BC008818; AAB08818.1; -
DR HSSP: P15692; 1VPF.
DR MIM: 601398; -.
DR InterPro: IPRO00072; PDGF.
DR Pfam: PF00341; PDGF; 1.
DR ProDom: PD001629; PDGF; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS00278; PDGF_2; 1.
DR KEGG: Growth factor; Glycoprotein; Signal; Heparin-binding;
KM Mitogen; Growth factor; Multigene family.
FT SIGNAL 1 21
FT CHAIN 22 207
FT DISULFID 47 89
FT DISULFID 62 122
FT DISULFID 72 124
FT DISULFID 81 81
FT DISULFID 137 188
FT VARSPLIC 137 188
FT FT
FT FT
FT FT
FT VARSPLIC 189 207
FT FT
FT FT
SQ SEQUENCE 207 AA; 21602 MW; EDE4B1C0DFDAD6BC CEC64;

Query Match 63.9%; Score 39; DB 1; Length 207;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERCG 10
DB 71 SCVTGRCG 79

RESULT 6
VEGB_MOUSE
ID VEGB_MOUSE STANDARD; PRT; 207 AA.
AC P49766; Q64290;
DT 01-OCT-1996 (Rel. 34; Created)
DT 01-MAR-2002 (Rel. 41; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE Vascular endothelial growth factor B precursor (VEGF-B) (VEGF related
factor) (VRF).

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GN VEGFB OR VRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS VEGF-B186 AND VEGF-B167).
RC TISSUE=Brain;
RX MEDLINE=96183052; PubMed=8607868;
RA Thompson S., Lagercrantz J., Grimmond S., Silins G., Nordenskjold M.,
RA Weber G., Hayward N.K.;
RL "Characterization of the murine VEGF-related factor gene.";
RL Biochem. Biophys. Res. Commun. 220:922-928(1996).
[2]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-B186).
RC TISSUE=Heart;
RX MEDLINE=96325041; PubMed=8702615;
RA Olofsson B., Paolusola K., von Euler G., Chillov D., Alltalo K.,
RA Eriksson U.;
RT "Genomic organization of the mouse and human genes for vascular
RT endothelial growth factor B (VEGF-B) and characterization of a second
RT splice isoform.";
RT J. Biol. Chem. 271:19310-19317(1996).
[3]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-B167).
RC TISSUE=Heart;
RX MEDLINE=96197355; PubMed=8637916;
RA Olofsson B.;
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
[4]
RP FUNCTION.
RX MEDLINE=21349816; PubMed=11457758;
RA Aase K., von Euler G., Li X., Ponten A., Thoren P., Cao R., Cao Y.,
RA Olofsson B., Gebre-Medhin S., Pekny M., Alltalo K., Betsholtz C.,
RA Eriksson U.;
RT "Vascular endothelial growth factor-B-deficient mice display an atrial
RT conduction defect.";
RT Circulation 104:358-364(2001).
[5]
RP -1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds
RP heparin and neuropilin-1 whereas the binding to neuropilin-1 of
RP VEGF-B186 is regulated by proteolysis. VEGF-B seems to be required
RP for normal heart function in adult but is not required for proper
RP development of the cardiovascular system either during development
RP or for angiogenesis in adults.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer
CC with vegf.
CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin.
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms: VEGF-B186 (shown here)
CC and VEGF-B167; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Abundantly expressed in heart, brain, kidney
CC and skeletal muscle.
CC -1- PTM: VEGF-B186 is O-glycosylated.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
DR EMBL: U43836; AAC52932.1; -
DR EMBL: U43837; AAC52553.1; -
DR EMBL: U52820; AAC52823.1; -
DR EMBL: U48800; AAB06273.1; -
DR HSSP: P15692; 2VGH.
DR MGD: MGI:106199; Vegfb.
DR InterPro: IPRO00072; PDGF.
DR Pfam: PF00341; PDGF; 1.

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us-09-471-459a-9\_1.rsp

DR	EMBL; D42123;	BAA07703.1;	-.
DR	EMBL; U36190;	AAB03194.1;	-.
DR	HSSP; P04006;	LIML.	
DR	MIM; 601183;	-.	
DR	InterPro; IPR001781;	LIM.	
DR	Pfam; PF00412;	LIM; 2.	
DR	PRODOM; PD000094;	LIM; 2.	
DR	SMART; SMO0132;	LIM; 2.	
DR	PROSITE; PS00478;	LIM_DOMAIN_1; 2.	
DR	PROSITE; PS50023;	LIM_DOMAIN_2; 2.	
KW	Repeat; LIM domain;	Metal-binding; zinc.	
FT	DOMAIN	5	LIM 1.
FT	DOMAIN	63	73 GLY-RICH.
FT	DOMAIN	126	178 LIM 2.
FT	DOMAIN	180	194 GLY-RICH.
SQ	SEQUENCE	208 AA;	22493 MW; D32B9FF98D51D3B0 CRC64;
Query March 60.7%; Score 37; DB 1; Length 208;			
Best Local Similarity 66.7%; Pred. NO. 11;			
Matches	6; Conservative	1; Mismatches	2; Indels
OY	3 CLIVERGE	11	0; Gaps
Db	150 CLRCRCK	158	

AC		09H2A7: (Rel. 41, Created)
DT	01-MAR-2002	(Rel. 41, Last sequence update)
DT	01-MAR-2002	(Rel. 41, Last annotation update)
DE	Small inducible cytokine B16 (Transmembrane chemokine CXCL16).	
GN	CXCL16.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	PubMed-11017100;	
RA	Melloujian M., David A., Engel S., Ryan J.E., Cyster J.G.;	
RT	"A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzoi"; Nat. Immunol. 1:298-304(2000).	
RL		
CC	-I- FUNCTION: Induces a strong chemotactic response. Induces calcium mobilization. Binds to CXCR6/Bonzo.	
CC	-I- SUBCELLULAR LOCATION: Type II membrane protein (potential). Also exist as a soluble form.	
CC	-I- TISSUE SPECIFICITY: Expressed in spleen, lymph nodes, lung, kidney, small intestine, and thymus; with weak expression in heart and liver and no expression in brain and bone marrow.	
CC	-I- PPM: Glycosylated.	
CC	-I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXC).	
CC		
CC	-----	
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .	
CC	-----	
DR	EMBL; AF301016; AAC34365.1; -.	
DR	MIY: 605398; -.	
DR	PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE NEG.	
FT	DATKIN: Chemotaxis; Transmembrane; Glycoprotein.	
FT	DOMAIN 1 29	
FT	TRANSREM 30 50	
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).	
FT	EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN 51 273	



CC Trp-1-Val-22 bond in the precursor.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC  
CC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.  
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CC -----  
DR EMBL: AB011176; BAA25530.1; -  
DR EMBL: AF192531; AAG28399.1; -  
DR HSSP: P08473; IDMT.  
DR MEROPS: M13.006; -  
DR InterPro: IPR000718; Peptidase\_M13.  
DR InterPro: IPR000130; Zn\_MTpeptidse.  
DR Pfam: PF01431; Peptidase\_M13; 1.  
DR PRINTS: PR00786; NEPRILYSIN.  
DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;  
KW Signal-anchor.  
FT DOMAIN 1 60 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 61 81 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT (POTENTIAL).  
FT DOMAIN 82 765 EXTRACELLULAR (POTENTIAL).  
FT METAL 602 602 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 603 603 BY SIMILARITY.  
FT METAL 606 606 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 662 662 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 666 666 PROTON DONOR (BY SIMILARITY).  
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 765 AA; 86469 MW; 89D1B831B5628694 CRC64;  
Query Match 57.4%; Score 35; DB 1; Length 765;  
Best Local Similarity 63.6%; Pred. No. 73;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
OY 1 MSCIMERGCE 11  
DB 179 LSCLOVERIEE 189  
RESULT 12  
ECEE2\_BOVIN STANDARD: PRT; 787 AA.  
AC 010711:  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).  
GN ECE2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95318093; PubMed=7797512;  
RA Emoto N., Yanagisawa M.;  
RT "Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon-  
sensitive metalloprotease with acidic pH optimum.";

RL J. Biol. Chem. 270:15262-15268(1995).  
CC -1- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1. OPTIMUM PH IS  
CC 5.5. INACTIVE AT NEUTRAL PH.  
CC -1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-  
CC Trp-1-Val-22 bond in the precursor.  
CC -1- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC  
CC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL: U27341; AAA82927.1; -  
DR HSSP: P08473; IDMT.  
DR MEROPS: M13.003; -  
DR InterPro: IPR000718; Peptidase\_M13.  
DR InterPro: IPR000130; Zn\_MTpeptidse.  
DR Pfam: PF01431; Peptidase\_M13; 1.  
DR PRINTS: PR00786; NEPRILYSIN.  
DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;  
KW Signal-anchor.  
FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 83 103 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT (POTENTIAL).  
FT DOMAIN 104 787 EXTRACELLULAR (POTENTIAL).  
FT METAL 624 624 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 625 625 BY SIMILARITY.  
FT METAL 628 628 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 684 684 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 688 688 PROTON DONOR (BY SIMILARITY).  
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 556 556 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 787 AA; 88957 MW; F085C2921DAF0BF2 CRC64;  
Query Match 57.4%; Score 35; DB 1; Length 787;  
Best Local Similarity 63.6%; Pred. No. 75;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
OY 1 MSCIMERGCE 11  
DB 201 LSCLOVERIEE 211  
RESULT 13  
GLTB\_AZOBOR STANDARD: PRT; 1515 AA.  
AC 005755:  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Glutamate synthase [NADPH] large chain precursor (EC 1.4.1.13)  
DE (Glutamate synthase alpha subunit) (NADPH-GOGAT) (GLTs alpha chain).  
GN GLTB.  
OS Azospirillum brasilense.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;  
OC Azospirillum.  
OX NCBI\_TaxID=192;

[1] SEQUENCE FROM N.A., AND SEQUENCE OF 37-56; 778-799 AND 1325-1345.  
RP STRAIN-SP7 / ATCC 29145;  
RC MEDLINE-93155143; PubMed-8428988;  
RX Pelanda R., Vannoni M.A., Perego M., Piubelli L., Galiezi A.,  
RA Curti B., Zanetti G.;  
RT "Glutamate synthase genes of the diazotroph Azospirillum brasilense.  
RT Cloning, sequencing, and analysis of functional domains.";  
RL J. Biol. Chem. 268:3099-3106(1993).  
[2]  
RP SEQUENCE OF 834-927 FROM N.A.  
RC STRAIN-RG;  
RX MEDLINE-94075244; PubMed-7902833;  
RA Mandal A.K., Ghosh S.;  
RT "Isolation of a glutamate synthase (GOGAT)-negative, pleiotropically  
RT N utilization-defective mutant of Azospirillum brasilense: cloning  
RT and partial characterization of GOGAT structural gene.";  
RL J. Bacteriol. 175:8024-8029(1993).  
[3]  
RP PARTIAL SEQUENCE.  
RX MEDLINE-90335272; PubMed-2198943;  
RA Vannoni M.A., Negri A., Zanetti G., Ronchi S., Curti B.;  
RT "Structural studies on the subunits of glutamate synthase from  
RT Azospirillum brasilense.";  
RL Biochim. Biophys. Acta 1039:374-377(1990).  
CC -1- CATALYTIC ACTIVITY: 2 L-glutamate + NADP(+) = L-glutamine + 2-  
CC oxoglutarate + NADPH.  
CC -1- COFACTOR: BINDS A 3FE-4S CLUSTER; FAD AND FMN.  
CC -1- PATHWAY: NITROGEN METABOLISM, GLUTAMATE BIOSYNTHESIS.  
CC THE CATALYZED REACTION BRINGS TOGETHER THE NITROGEN AND  
CC CARBON METABOLISM.  
CC -1- SUBUNIT: AGGREGATE OF 4 CATALYTICAL ACTIVE HETEROIMERS,  
CC CONSISTING OF A LARGE AND A SMALL SUBUNIT.  
CC -1- MISCELLANEOUS: GLUTAMINE BINDS TO THE LARGE SUBUNIT AND TRANSFERS  
CC THE AMINO GROUP TO 2-OXO-GLUTAMATE THAT APPARENTLY BINDS TO THE  
CC SMALL SUBUNIT.  
CC -1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.  
-----  
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DR EMBL: AF192408; AAA22179.1; -;  
DR EMBL: X71632; CAA50639.1; -;  
DR PIR: B46602; B46602.  
DR InterPro: IPR002489; DUF14.  
DR InterPro: IPR003009; FMN enzyme.  
DR InterPro: IPR002932; Glu synthase.  
DR Pfam: PF01493; DUF14.1.  
DR Pfam: PF01645; Glu synthase; 1.  
DR Oxidoreductase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NADP;  
KW Glutamate biosynthesis; Zymogen.  
FT PROPEP 37 1515  
FT CHAIN 37 1515  
FT NP\_BIND 1085 1142  
FT METAL 1138 1142  
FT METAL 1144 1144  
FT METAL 1149 1149  
FT NP\_BIND 1086 1142  
SQ SEQUENCE 1515 AA; 166018 MW; ED913218BFCFE92 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 1515;  
Best Local Similarity 55.6%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSCIWERC 9  
DB 1136 MGCIVROC 1144

RESULT 14  
ID GLT1\_YEAST  
AC 012680; Q12290;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Glutamate synthase [NADPH] precursor (RC 1.4.1.13) (NADPH-GOGAT).  
GN GLT1 OR YDL171C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC STRAIN-CN36;  
RX MEDLINE-97082505; PubMed-8923741.  
RA Elieci P., Martegani M.P., Valenzuela L., Gonzalez A., Ballario P.;  
RT "Sequence of the GLT1 gene from Saccharomyces cerevisiae reveals the  
RT domain structure of yeast glutamate synthase.";  
RL Yeast 12:1359-1366(1996).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C;  
RA Pohl T.M.;  
RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: 2 L-glutamate + NADP(+) = L-glutamine + 2-  
CC oxoglutarate + NADPH.  
CC -1- COFACTOR: BINDS A 3FE-4S CLUSTER; FAD AND FMN.  
CC -1- SUBUNIT: HOMOTRIMER.  
CC -1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.  
-----  
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-----  
DR EMBL: X89221; CAA61505.1; -;  
DR EMBL: Z67750; CAA91574.1; -;  
DR EMBL: Z74219; CAA98745.1; -;  
DR SCD: S0002330; GLT1.  
DR InterPro: IPR002489; DUF14.  
DR InterPro: IPR001327; FAD pyr redox.  
DR InterPro: IPR002932; Glu synthase.  
DR Pfam: PF01493; DUF14.1.  
DR Pfam: PF01645; Glu synthase; 1.  
DR Pfam: PF00070; Pyr redox; 1.  
DR Oxidoreductase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NADP;  
KW Glutamate biosynthesis; Zymogen.  
FT PROPEP 1 53  
FT CHAIN 1 53  
FT NP\_BIND 1131 1144  
FT METAL 1184 1184  
FT METAL 1190 1190  
FT METAL 1195 1195  
FT CONFLICT 30 30  
FT CONFLICT 166 172  
FT CONFLICT 449 451  
FT CONFLICT 1752 1752  
SQ SEQUENCE 2144 AA; 238200 MW; 5AA6A948EF95349 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 2144;  
Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSCIWERC 9  
DB 1182 MGCVMRLRC 1190



Mon Oct 28 10:52:07 2002

2 . . 3

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RESULT 15
CRP1_HUMAN
ID CRP1_HUMAN STANDARD; PRT; 76 AA.
AC P50238; Q13628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cysteine-rich protein 1 (Cysteine-rich intestinal protein) (CRIP)
DE (Cysteine-rich heart protein) (hCRHP).
GN CRIP OR CRIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95091772; PubMed=7999070;
RA Tsui S.K., Yam N.Y., Lee C.Y., Maye M.M.;
RT "Isolation and characterization of a cDNA that codes for a LIM-
RT containing protein which is developmentally regulated in heart.";
RL Blochem. Biophys. Res. Commun. 205:497-505(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=97271694; PubMed=9126610;
RA Khoo C., Blanchard R.K., Sullivan V.K., Cousins R.J.;
RT "Human cysteine-rich intestinal protein: cDNA cloning and expression
RT of recombinant protein and identification in human peripheral blood
RT mononuclear cells.";
RL Protein Expr. Purif. 9:379-387(1997).
CC -!- FUNCTION: SEEMS TO HAVE A ROLE IN ZINC ABSORPTION AND MAY FUNCTION
CC AS AN INTRACELLULAR ZINC TRANSPORT PROTEIN.
CC -!- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2
CC ZINC IONS.
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CC -----
DR EMBL; U09770; AAA64537.1; -
DR EMBL; U58630; AAB61158.1; -
DR HSSP; P04006; IIML.
DR MIM; 123875; -
DR InterPro: IPR001781; LIM.
DR Pfam; PF00412; LIM; 1.
DR ProDom; PD000094; LIM; 1.
DR SMART; SM00132; LIM; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; 1.
DR PROSITE; PS50023; LIM_DOMAIN_2; 1.
KW LIM domain; Metal-binding; Zinc.
FT INIT_MET 0 BY SIMILARITY.
FT DOMAIN 3 LIM.
FT DOMAIN 60 LIM.
FT DOMAIN 61 GLY-RICH.
FT CONFLICT 57 V -> A (IN REF. 2).
SQ SEQUENCE 76 AA; 8430 MW; ECC3737CF0EDF97E CRC64;

Query Match 55.7%; Score 34; DB 1; Length 76;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CLAMERGE 11
DB 27 CLKCKCKG 35

```

Search completed: October 27, 2002, 09:22:00  
 Job time : 28 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 27, 2002, 08:19:12 : Search time 69 seconds  
(without alignments)  
27.579 Million cell updates/sec

Title: US-09-471-459A-9  
Perfect score: 61  
Sequence: 1 MSCLMVERGE 11

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_trembl\_19:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_riccia:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	67.2	290	11 Q9D1L8	Q9D1L8 mus musculu
2	41	67.2	364	4 Q9BHV5	Q9BHV5 homo sapien
3	41	67.2	370	4 Q9GZP0	Q9GZP0 homo sapien
4	41	67.2	370	11 Q9E0T1	Q9E0T1 rattus norv
5	41	67.2	370	11 Q9Z517	Q9Z517 mus musculu
6	40	65.6	345	4 Q9NRAL	Q9NRAL homo sapien
7	40	65.6	345	4 Q9UL22	Q9UL22 homo sapien
8	40	65.6	345	11 Q9E0X6	Q9E0X6 rattus norv
9	40	65.6	345	11 Q9JHV8	Q9JHV8 mus musculu
10	40	65.6	345	11 Q9QY71	Q9QY71 mus musculu
11	40	65.6	345	13 Q9I946	Q9I946 gallus galli
12	40	65.6	1583	10 Q9LR38	Q9LR38 arabidopsis
13	38	62.3	213	4 Q9NSM1	Q9NSM1 homo sapien
14	38	62.3	349	5 Q9N8U9	Q9N8U9 trypanosoma
15	38	62.3	517	10 Q49386	Q49386 arabidopsis
16	37	60.7	366	5 Q22627	Q22627 caenorhabdi

17	37	60.7	626	10 Q9M548	Q9M548 arabidopsis
18	37	60.7	652	5 Q19447	Q19447 caenorhabdi
19	37	60.7	1531	2 Q9RN27	Q9RN27 zymomonas m
20	37	60.7	1545	2 Q9RNL3	Q9RNL3 zymomonas m
21	36	59.0	254	4 Q9H2F6	Q9H2F6 homo sapien
22	36	59.0	254	4 Q9BXD6	Q9BXD6 homo sapien
23	36	59.0	261	6 Q9SLN6	Q9SLN6 macaca fasc
24	36	59.0	273	4 Q96K63	Q96K63 macaca fasc
25	36	59.0	343	2 Q9KJN9	Q9KJN9 myxococcus
26	36	59.0	596	6 Q9GMA7	Q9GMA7 macaca fasc
27	36	59.0	693	13 Q9DGC5	Q9DGC5 oreochromis
28	36	59.0	696	13 Q9RT85	Q9RT85 ictalurus p
29	36	59.0	697	4 Q9Y4M9	Q9Y4M9 homo sapien
30	36	59.0	1071	10 Q9C607	Q9C607 arabidopsis
31	36	59.0	1071	12 Q9Y2A1	Q9Y2A1 gallid herp
32	36	59.0	1224	10 Q9C728	Q9C728 arabidopsis
33	36	59.0	1225	10 Q9Z0F8	Q9Z0F8 arabidopsis
34	36	59.0	1272	4 Q9HAU5	Q9HAU5 homo sapien
35	36	59.0	1272	4 Q9H1J2	Q9H1J2 homo sapien
36	36	59.0	1298	4 Q9P2D9	Q9P2D9 homo sapien
37	35	57.4	255	10 Q9LXE6	Q9LXE6 equine herp
38	35	57.4	302	12 Q6651	Q6651 equine herp
39	35	57.4	303	12 Q9YTP6	Q9YTP6 ateline her
40	35	57.4	346	5 Q9NPF21	Q9NPF21 calliphora
41	35	57.4	354	10 Q9FG55	Q9FG55 arabidopsis
42	35	57.4	378	12 Q65822	Q65822 bovine herp
43	35	57.4	391	10 P92929	P92929 antihemio
44	35	57.4	463	2 Q07346	Q07346 synechocyst
45	35	57.4	463	16 P73374	P73374 synechocyst

## ALIGNMENTS

RESULT 1	ID	Q9D1L8	PRELIMINARY:	PRT:	290 AA.
AC	Q9D1L8	01-JUN-2001 (TREMREL. 17, Created)			
DT	01-JUN-2001 (TREMREL. 17, Last sequence update)				
DE	01-DEC-2001 (TREMREL. 19, Last annotation update)				
DN	1110003109R1K PROTEIN.				
GN	1110003109R1K.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_Taxid=10090;					
RP	[1]				
RC	SEQUENCE FROM N.A.				
RA	STRAIN=C57BL/6J; TISSUE=EMBRYO;				
RA	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gliszi C., King B., Kochiwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombarts P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Williams L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,				
RA	Hayashizaki Y.,				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
CC	-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.				
DR	EMBL, AK003359; BAB22735.1; -				



OS Rattus norvegicus (rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21092670; PubMed=11162582;  
RA Hamada T., U-Tel K., Imaki J., Miyata Y.;  
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to  
RT SCDGF/PDGF-C/Fallotelin.";  
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL: AB052170; BAB18920.1; -.  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR000072; PDGF.  
DR Pfam: PF00431; CUB; 1.  
DR SMART: SM00042; CUB; 1.  
DR SMART: SM00141; PDGF; 1.  
DR PROSITE: PS01180; CUB; 1.  
DR PROSITE: PS50278; PDGF\_2; 1.  
SQ SEQUENCE 370 AA; 42809 MW; 7BB8A251F679BF73 CRC64;

Query Match 67.2%; Score 41; DB 11; Length 370;  
Best Local Similarity 75.0%; Pred. No. 7.3;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLMVERCG 10  
Db 296 CLVORCG 303

RESULT 5  
O92517 PRELIMINARY; PRT; 370 AA.  
AC O92517;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PLATELET-DERIVED GROWTH FACTOR D.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA1B/C;  
RX MEDLINE=21231380; PubMed=11331882;  
RA Larocheille W.J., Jeffers M., McDonald W.F., Chhilaikuru R.A.,  
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,  
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkels J.,  
RA Shinkels R.A., Rothberg J.M., Lichenstein H.S.;  
RT "PDGF D, A Novel Protease-Activated Growth Factor.";  
RL Nat. Cell Biol. 3:517-521(2001).  
DR EMBL: AF335583; AAK38839.1; -.  
SQ SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;

Query Match 67.2%; Score 41; DB 11; Length 370;  
Best Local Similarity 75.0%; Pred. No. 7.3;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLMVERCG 10  
Db 296 CLVORCG 303

RESULT 6  
O9NRA1 PRELIMINARY; PRT; 345 AA.  
ID O9NRA1;  
AC O9NRA1;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
RL PLATELET-DERIVED GROWTH FACTOR C.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LUNG;  
RX MEDLINE=20268201; PubMed=10806482;  
RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,  
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,  
RA Besholtz C., Heidin C.-H., Alltalo K., Ostman A., Eriksson U.;  
RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-  
RT receptor.";  
RL Nat. Cell Biol. 2:302-309(2000).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL: AF244813; AAF80597.1; -.  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR000072; PDGF.  
DR Pfam: PF00431; CUB; 1.  
DR Pfam: PF00341; PDGF; 1.  
DR SMART: SM00042; CUB; 1.  
DR SMART: SM00141; PDGF; 1.  
DR PROSITE: PS01180; CUB; 1.  
DR PROSITE: PS50278; PDGF\_2; 1.  
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 65.6%; Score 40; DB 4; Length 345;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLMVERCG 10  
Db 274 CLVORCG 281

RESULT 7  
O9UL22 PRELIMINARY; PRT; 345 AA.  
ID O9UL22;  
AC O9UL22;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTELIN (SPINAL CORD-DERIVED  
DE GROWTH FACTOR) (PLATELET-DERIVED GROWTH FACTOR C).  
GN HSCDGF OR PDGFC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UTERUS;  
RA Tsai Y.-J., Lee R.K.K., Lin S.P.;  
RT "Fallotelin, a novel growth factor like gene identified in human  
RT uterus.";  
RL Submitted (SEP-1998) to the EMBL/genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=20317014; PubMed=10858496;  
RA Hamada T., U-Tel K., Miyata Y.;  
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique  
RT member of the PDGF/VEGF family.";  
RL FEBS Lett. 475:97-102(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21347863; PubMed=11297552;  
RA Gilbertson D.C., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,  
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,  
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;  
RT "Platelet-derived growth factor C (PDGF-C), a Novel Growth Factor That  
RT Binds to PDGF alpha and beta Receptor.";  
RL J. Biol. Chem. 276:27406-27414(2001).

Query Match 65.6%; Score 40; DB 4; Length 345;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL: AF091434; AAF00049.1; -  
DR EMBL: AB033831; BAB03266.1; -  
DR EMBL: AF260738; AAK51637.1; -  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR00072; PDGF.  
DR Pfam: PF00431; CUB; 1.  
DR Pfam: PF00341; PDGF; 1.  
DR SMART: SM00042; CUB; 1.  
DR SMART: SM00141; PDGF; 1.  
DR PROSITE: PS01180; CUB; 1.  
DR PROSITE: PS50278; PDGF\_2; 1.  
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 65.6%; Score 40; DB 4; Length 345;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CLIVERCG 10  
||:|:|:|  
Db 274 CLIVKRCG 281

## RESULT 8

O9EOX6 PRELIMINARY; PRT; 345 AA.  
AC O9EOX6:  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE SPINAL CORD-DERIVED GROWTH FACTOR.  
GN RSCDGF.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISTAR; TISSUE=KIDNEY;  
RX MEDLINE=21092670; PubMed=11162582;  
RA Hamada T., U-Tel K., Imaki J., Miyata Y.;  
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to  
RT SCDF/PDGF-C/falotin.";  
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL: AB033830; BAB19969.1; -  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR00072; PDGF.  
DR Pfam: PF00431; CUB; 1.  
DR SMART: SM00042; CUB; 1.  
DR SMART: SM00141; PDGF; 1.  
DR PROSITE: PS01180; CUB; 1.  
DR PROSITE: PS50278; PDGF\_2; 1.  
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 65.6%; Score 40; DB 11; Length 345;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CLIVERCG 10  
||:|:|:|  
Db 274 CLIVKRCG 281

## RESULT 9

O9JHV8 PRELIMINARY; PRT; 345 AA.  
AC O9JHV8:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PLATELET-DERIVED GROWTH FACTOR C.  
GN PDGFC.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SWISS-WEBSTER/NIH;  
RX MEDLINE=20417814; PubMed=10960785;  
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;  
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during  
RT organogenesis.";  
RL Mech. Dev. 96:209-213(2000).  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL: AF286725; AAF91483.1; -  
DR MGD: MGI:1859631; pdgfc.  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR00072; PDGF.  
DR Pfam: PF00431; CUB; 1.  
DR SMART: SM00042; CUB; 1.  
DR SMART: SM00141; PDGF; 1.  
DR PROSITE: PS01180; CUB; 1.  
DR PROSITE: PS50278; PDGF\_2; 1.  
SQ SEQUENCE 345 AA; 38886 MW; FA1486BEDD362F8 CRC64;

Query Match 65.6%; Score 40; DB 11; Length 345;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CLIVERCG 10  
||:|:|:|  
Db 274 CLIVKRCG 281

## RESULT 10

O9QY71 PRELIMINARY; PRT; 345 AA.  
AC O9QY71:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE FALLOTEIN (PLATELET-DERIVED GROWTH FACTOR C).  
GN PDGFC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY.  
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;  
RT "cDNA cloning of falloletin from mouse ovary";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,  
RT Gilbertson D., West J., O'Hara P.J.;  
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that  
RT binds to PDGF alpha receptor.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL: AF117608; AAF22516.1; -  
DR EMBL: AF264647; AAK58566.1; -  
DR MGD: MGI:1859631; pdgfc.  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR00072; PDGF.  
DR Pfam: PF00431; CUB; 1.  
DR SMART: SM00042; CUB; 1.  
DR SMART: SM00141; PDGF; 1.  
DR PROSITE: PS01180; CUB; 1.  
DR PROSITE: PS50278; PDGF\_2; 1.  
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

Query Match 65.6%; Score 40; DB 11; Length 345;  
 Best Local Similarity 75.0%; Pred. No. 11;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLMVERCG 10  
 11:1111  
 Db 274 CLMVERCG 281

## RESULT 11

O91946 PRELIMINARY; PRT; 345 AA.  
 AC O91946;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE SPINAL CORD-DERIVED GROWTH FACTOR.  
 GN SCDF.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WHITE LEHORN; TISSUE=SPINAL CORD;  
 RX MEDLINE=20317014; PubMed=10858496;  
 RA Hamada T., U-Tel K., Miyata Y.;  
 RT "A novel gene derived from developing spinal cords, SCDF, is a unique  
 member of the PDGF/VEGF family.";  
 RL FEBS Lett. 475:97-102(2000).  
 CC 1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL: AB033829; BAB03265.1; -;  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR000072; PDGF.  
 DR Pfam: PF00431; CUB; 1.  
 DR SMART: SM00042; CUB; 1.  
 DR SMART: SM00141; PDGF; 1.  
 DR SMART: PS01180; CUB; 1.  
 DR PROSITE: PS00278; PDGF\_2; 1.  
 DR PROSITE: PS00278; PDGF\_2; 1.  
 SQ SEQUENCE 345 AA; 38940 MW; 97ACEA92BF5128C CRC64;

Query Match 65.6%; Score 40; DB 13; Length 345;  
 Best Local Similarity 75.0%; Pred. No. 11;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLMVERCG 10  
 11:1111  
 Db 274 CLMVERCG 281

## RESULT 12

O91R38 PRELIMINARY; PRT; 1583 AA.  
 AC O91R38;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE P26F24.8.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eusids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Gasser C.S.,  
 RA Khan S., Kim C., Shin P., Villanueva J.M., Altafi H., Bel O.,  
 RA Chin C., Chou J., Choi E., Conn L., Conway A., Gonzales A.,  
 RA Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A.,  
 RA Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H.,  
 RA Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G.,  
 RA Federspiel N.A., Theologis A., Ecker J.R.;

RT "Genomic sequence for Arabidopsis thaliana BAC F26F24 from chromosome  
 1.";  
 RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RN Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RN 13  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN 14  
 RP SEQUENCE FROM N.A.  
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN 15  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altafi H., Bel O., Chin C., Chou J., Choi E.,  
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Theologis A., Ecker J.;  
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC005292; AAF86997.1; -;  
 SQ SEQUENCE 1583 AA; 176638 MW; 84882A269E8A47D1 CRC64;

Query Match 65.6%; Score 40; DB 10; Length 1583;  
 Best Local Similarity 50.0%; Pred. No. 40;  
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSCLMVERCG 10  
 11:1111  
 Db 1349 LSCLLIQACG 1358

## RESULT 13

O9NSM1 PRELIMINARY; PRT; 213 AA.  
 AC O9NSM1;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HYPOTHETICAL 21.9 KDA PROTEIN (FRAGMENT).  
 GN DKFZF61L0812.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=AMYGDALA;  
 RA Ansgorge W., Winkner U., Mewes H.W., Weil B., Wiemann S.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL162044; CAB82387.1; -;  
 KM Hypothetical protein.  
 FT NON-TER  
 SQ SEQUENCE 213 AA; 21903 MW; CE76895FE1F22A4A CRC64;

Query Match 62.3%; Score 38; DB 4; Length 213;  
 Best Local Similarity 77.8%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 SCLMVERCG 10  
 11:1111  
 Db 15 SCLMVERCG 23

RESULT 14  
 O9NB39 PRELIMINARY; PRT; 349 AA.  
 AC O9NB39;  
 OX O9NB39;

DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE HYPOTHETICAL 39.1 KDA PROTEIN.  
 GN CHRL303.  
 OS Trypanosoma brucei.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5691;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TREU927;  
 RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,  
 RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,  
 RA Gerard C., Rajandream M.A., Barrell B.G.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL359782; CAB95544.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 349 AA; 39078 MW; 934417B9A6DA107C CRC64;

Query Match 62.3%; Score 38; DB 5; Length 349;  
 Best Local Similarity 50.0%; Pred. No. 25;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSCLWVRGCG 10  
 DB 169 LSCVRSRCG 178

RESULT 15  
 ID 049386 PRELIMINARY; PRT. 517 AA.  
 AC 049386;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1999 (TREMBLrel. 09, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE HYPOTHETICAL 57.1 KDA PROTEIN.  
 GN F10N7.130 OR ATAG32050.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Koeltter P., Hempel S., Entian K.-D., Hohenseil J.,  
 RA Mewes H.W., Meyer K.F.X., Scheller C.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Meyer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL021636; CAI16583.1; -  
 DR EMBL; AL161580; CAB95923.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 517 AA; 57106 MW; 11503D5E4ECB3DDA CRC64;

Query Match 62.3%; Score 38; DB 10; Length 517;  
 Best Local Similarity 53.8%; Pred. No. 36;  
 Matches 7; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

OY 1 MSCL--NVRGCG 11  
 DB 478 VECLIKLIERGCG 490

Search completed: October 27, 2002, 09:23:32  
 Job time : 73 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2002, 07:14:41 ; Search time 53 Seconds  
(without alignments)  
6270.606 Million cell updates/sec

Title: US-09-471-459A-6

Perfect score: 1353

Sequence: 1 atgcttggttaatggttga.....aggaagcgacagccctag 1353

Scoring table: IDENTITY\_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.NA:\*  
1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2.6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2.6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2.6/ptodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgn2.6/ptodata/1/ina/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1273.6	94.1	2201	US-09-330-970-2	Sequence 2, Appl
2	723.8	53.5	3336	US-09-330-970-4	Sequence 4, Appl
3	500.6	37.0	3987	US-07-688-352C-19	Sequence 19, Appl
4	500.6	37.0	3987	US-08-474-379C-19	Sequence 19, Appl
5	500.6	37.0	3987	US-09-146-249A-19	Sequence 19, Appl
6	500.6	37.0	3987	US-08-206-188B-19	Sequence 19, Appl
7	500.6	37.0	3987	US-09-146-249A-19	Sequence 19, Appl
8	120.2	8.9	2158	US-07-688-352C-3	Sequence 3, Appl
9	120.2	8.9	2158	US-08-474-379C-3	Sequence 3, Appl
10	120.2	8.9	2158	US-09-146-249A-3	Sequence 3, Appl
11	120.2	8.9	2158	US-08-206-188B-3	Sequence 3, Appl
12	120.2	8.9	2158	PCT-US91-02714-3	Sequence 3, Appl
13	105	7.8	2178	US-08-474-379C-80	Sequence 80, Appl
14	105	7.8	2178	US-09-146-249A-80	Sequence 80, Appl
15	105	7.8	2178	US-08-206-188B-80	Sequence 80, Appl
16	105	7.8	2178	US-08-474-379C-82	Sequence 82, Appl
17	105	7.8	2178	US-09-146-249A-82	Sequence 82, Appl
18	105	7.8	2178	US-08-206-188B-82	Sequence 82, Appl
19	103.8	7.7	1902	US-07-688-352C-43	Sequence 43, Appl
20	103.8	7.7	1902	US-08-474-379C-43	Sequence 43, Appl
21	103.8	7.7	1902	US-09-146-249A-43	Sequence 43, Appl
22	103.8	7.7	1902	US-08-206-188B-43	Sequence 43, Appl
23	103.8	7.7	1902	PCT-US91-02714-40	Sequence 40, Appl
24	103.8	7.7	1902	US-07-688-352C-21	Sequence 21, Appl
25	103.8	7.7	1902	US-09-146-249A-21	Sequence 21, Appl
26	103.8	7.7	1902	US-08-206-188B-21	Sequence 21, Appl
27	103.8	7.7	1902	PCT-US91-02714-20	Sequence 20, Appl

28	99.4	7.3	3186	US-07-688-352C-23	Sequence 23, Appl
29	99.4	7.3	3186	US-08-474-379C-23	Sequence 23, Appl
30	99.4	7.3	3186	US-09-146-249A-23	Sequence 23, Appl
31	99.4	7.3	3186	US-08-206-188B-23	Sequence 23, Appl
32	99.4	7.3	3186	PCT-US91-02714-22	Sequence 22, Appl
33	99.4	7.3	3890	US-08-942-521B-1	Sequence 1, Appl
34	99.4	7.3	3890	US-09-192-702-1	Sequence 1, Appl
35	99.4	7.3	3890	US-08-445-474-1	Sequence 1, Appl
36	99.4	7.3	3890	PCT-US94-02612-1	Sequence 1, Appl
37	99.4	7.3	4068	US-08-474-379C-58	Sequence 58, Appl
38	99.4	7.3	4068	US-09-146-249A-58	Sequence 58, Appl
39	99.4	7.3	4068	US-08-206-188B-58	Sequence 58, Appl
40	99.4	7.3	2077	US-07-872-644-52	Sequence 52, Appl
41	98.4	7.3	2077	US-08-297-510-52	Sequence 52, Appl
42	98.4	7.3	2077	US-08-479-532-52	Sequence 52, Appl
43	98.4	7.3	2077	US-08-455-526-52	Sequence 52, Appl
44	98.4	7.3	2077	US-08-455-526-52	Sequence 52, Appl
45	98.4	7.3	2077	US-08-455-526-52	Sequence 52, Appl

## ALIGNMENTS

RESULT 1  
US-09-330-970-2  
; Sequence 2, Application US/09330970  
; Patent No. 6146876  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: White, David  
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide  
; FILE REFERENCE: 5800-28  
; CURRENT FILING DATE: 1999-06-11  
; EARLIER APPLICATION NUMBER: 09/277,423  
; EARLIER FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 2201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (224)...(1729)  
US-09-330-970-2

Query Match 94.1%; Score 1273.6; DB 3; Length 2201;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1276; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	74	GCATGCTGGAGATATACACTAAGGCGGCGACAGCGGGGCTGCTGTAAGCGCGTGGCT	133
DB	453	GCTTTCAGAGATATACACTAAGGCGGCTGACAGCGGGGCTGCTGTAAGCGCGTGGCT	512
QY	134	CTTACCATTCATTCGCTCCGCTTACTTAACAGTCAACATCTAGGAGATTGGCA	193
DB	513	CTTACCATTCATTCGCTCCGCTTACTTAACAGTCAACATCTAGGAGATTGGCA	572
QY	194	CCAAGAAAAAGTGAAAGACTTAAAGCTTCAAGATACCTTCATCAAGGCTGC	253
DB	573	CCAAGAAAAAGTGAAAGACTTAAAGCTTCAAGATACCTTCATCAAGGCTGC	632
QY	254	TTGCGTGAATTTATACCAAGGCGGCTGCTGCTGATGAAGCTGCTGGACAG	313
DB	633	TTGCGTGAATTTATACCAAGGCGGCTGCTGCTGATGAAGCTGCTGGACAG	692
QY	314	CAAGCATATGCTCTCCAAAGTGGAGATGGGATTTGACATTTCTTGTGATCGCT	373
DB	693	CAAGCATATGCTCTCCAAAGTGGAGATGGGATTTGACATTTCTTGTGATCGCT	752

OY 374 TGACAAATGGAACAGCCTGTAACACTGTGTGCCACCTCTTCAATACCATGAGACTCA 433  
 Db 753 TGACAAATGGAACAGCCTGTAACACTGTGTGCCACCTCTTCAATACCATGAGACTCA 812  
 OY 434 TTCAACATTTCAAGTTAGATATGATGACCTTTACACCCGATTTTATGATGATGATGATG 493  
 Db 813 TTCAACATTTCAAGTTAGATATGATGACCTTTACACCCGATTTTATGATGATGATGATG 872  
 OY 494 ATTACCAAGCAAAACCCGATATCAATGCTTTACACCCGATGATGATGATGATGATGATG 553  
 Db 873 ATTACCAAGCAAAACCCGATATCAATGCTTTACACCCGATGATGATGATGATGATGATG 932  
 OY 554 TGCACCTGCTACCTGTAAGAGCAAGGCTTCCGAGCTTCTCAGCCTCTGAGCAATCAAGC 613  
 Db 933 TGCACCTGCTACCTGTAAGAGCAAGGCTTCCGAGCTTCTCAGCCTCTGAGCAATCAAGC 992  
 OY 614 TTGACACCTGCTGCTGACAGCAGCAGATGTGACACCCAGGAGGTAACACGACCATTTT 673  
 Db 993 TTGACACCTGCTGCTGACAGCAGCAGATGTGACACCCAGGAGGTAACACGACCATTTT 1052  
 OY 674 TGATPAAAACTAACACCATCTTTGCAAAACCTATATCAGAAATATGTCTGTGTGAGAAATC 733  
 Db 1053 TGATPAAAACTAACACCATCTTTGCAAAACCTATATCAGAAATATGTCTGTGTGAGAAATC 1112  
 OY 734 ATCACTGCGCATCTACAAATTTGGCATGCTTGCAGAAATCAAGGCTTCTGTCTATTTGCCAA 793  
 Db 1113 ATCACTGCGCATCTACAAATTTGGCATGCTTGCAGAAATCAAGGCTTCTGTCTATTTGCCAA 1172  
 OY 794 AGGAATGACACAGGATATTTGAACAGCAGCTGGGCTCTTGTATCTTGGCAACAGACATCA 853  
 Db 1173 AGGAATGACACAGGATATTTGAACAGCAGCTGGGCTCTTGTATCTTGGCAACAGACATCA 1232  
 OY 854 ACAGGCAAGTGAATTTTGTACAGATTTGAAGCTCAGCTCAGCAATTAAGCTTAACAC 913  
 Db 1233 ACAGGCAAGTGAATTTTGTACAGATTTGAAGCTCAGCTCAGCAATTAAGCTTAACAC 1292  
 OY 914 TGGAGATGACAGGAGGACCTTATGCTTCAAGTGGCTTGAAGGCTGCTGACATTT 973  
 Db 1293 TGGAGATGACAGGAGGACCTTATGCTTCAAGTGGCTTGAAGGCTGCTGACATTT 1352  
 OY 974 GCATCTCTTGAATTTGGAAGATGAGCAAGCAGTGGAGTGAAGGCTGTGTGAAGAT 1033  
 Db 1353 GCATCTCTTGAATTTGGAAGATGAGCAAGCAGTGGAGTGAAGGCTGTGTGAAGAT 1412  
 OY 1034 TCTACAGGCAAGTGAATTTGAACAGAAATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1093  
 Db 1413 TCTACAGGCAAGTGAATTTGAACAGAAATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1472  
 OY 1094 AACGAAAGATTTCCATCTCTAGATATCAAAATTTGATTTCTAGATATCTGTGAGCCG 1153  
 Db 1473 AACGAAAGATTTCCATCTCTAGATATCAAAATTTGATTTCTAGATATCTGTGAGCCG 1532  
 OY 1154 TCTTCCGCGAATGGCCCATTTTACGCGGTAAAGCAGCCTGTGCGAGAAATGTGTGCGCC 1213  
 Db 1533 TCTTCCGCGAATGGCCCATTTTACGCGGTAAAGCAGCCTGTGCGAGAAATGTGTGCGCC 1592  
 OY 1214 ACCTCGCAGCAACAAAGGCGCATGTAAGAGGCTGTGCGAGGAGAGCAAGCAAGG 1273  
 Db 1593 ACCTCGCAGCAACAAAGGCGCATGTAAGAGGCTGTGCGAGGAGAGCAAGCAAGG 1652  
 OY 1274 GCAGCAGTGGCAGGCGCGTGAACAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1333  
 Db 1653 GCAGCAGTGGCAGGCGCGTGAACAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1712  
 OY 1334 AGGAAGGCGACAGCCCTAG 1353  
 Db 1713 AGGAAGGCGACAGCCCTAG 1732

RESULT 2  
 US-09-330-970-4  
 ; Sequence 4, Application US/09330970  
 ; Patent No. 6146876

; GENERAL INFORMATION:  
 ; APPLICANT: Robison, Keith E.  
 ; APPLICANT: Kapeller-Libermann, Rosana  
 ; APPLICANT: White, David  
 ; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide  
 ; TITLE OF INVENTION: Phosphodiesterase  
 ; FILE REFERENCE: 5800-28  
 ; CURRENT APPLICATION NUMBER: US/09/330,970  
 ; EARLIER FILING DATE: 1999-06-11  
 ; EARLIER APPLICATION NUMBER: 09/277,423  
 ; EARLIER FILING DATE: 1998-03-26  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 3336  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc-feature  
 ; LOCATION: (1)...(3336)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-330-970-4  
 Query Match 53.5%; Score 723.8; DB 3; Length 3336;  
 Best Local Similarity 99.0%; Pred. No. 1.3e-205;  
 Matches 728; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 OY 74 GCATGCTGAGATATPACACTAAGGGGTGACAGAGGGGTTGCTGGAACGGCGTGGCT 133  
 Db 452 GCTTCCAGAGATATPACACTAAGGGGTGACAGAGGGGTTGCTGGAACGGCGTGGCT 511  
 OY 134 CCTACCATTTCTTACTCTCCGCTACTTAACATACATCTCAGGAGGATTTGGA 193  
 Db 512 CCTACCATTTCTTACTCTCCGCTACTTAACATACATCTCAGGAGGATTTGGA 571  
 OY 194 CCAAAAAAGGTGAAGAGTATTAAGCTTTCAAAATCTTCCATGATCAAGGCTGC 253  
 Db 572 CCAAAAAAGGTGAAGAGTATTAAGCTTTCAAAATCTTCCATGATCAAGGCTGC 631  
 OY 254 TTGCTGGAATTTACACACAGCCCTCTGCACTGCTGATGAAGACTTCTTGAACAG 313  
 Db 632 TTGCTGGAATTTACACACAGCCCTCTGCACTGCTGATGAAGACTTCTTGAACAG 691  
 OY 314 CAAGCATATGCTCTCCAAAGTGGGAATGTGGATTTTGAATTTCTTGTGTGATGCT 373  
 Db 692 CAAGCATATGCTCTCCAAAGTGGGAATGTGGATTTTGAATTTCTTGTGTGATGCT 751  
 OY 374 TGACAAATGGAACAGCCTGTAACACTGTTGCGCACCTCTTCAATACCATGAGACTCA 433  
 Db 752 TGACAAATGGAACAGCCTGTAACACTGTTGCGCACCTCTTCAATACCATGAGACTCA 811  
 OY 434 TTCAACATTTCAAGTTAGATATGATGACCTTTACACCCGATTTTATGATGATGATG 493  
 Db 812 TTCAACATTTCAAGTTAGATATGATGACCTTTACACCCGATTTTATGATGATGATG 871  
 OY 494 ATTACCAAGCAAAACCCGATATCAATGCTTTACACCCGATGATGATGATGATGATG 553  
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 OY 554 TGCACCTGCTACCTGTAAGAGCAAGGCTTCCGAGCTTCTCAGCCTCTGAGCAATCAAGC 613  
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 OY 614 TTGACACCTGCTGCTGACAGCAGCAGATGTGACACCCAGGAGGTAACACGACCATTTT 673  
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 OY 674 TGATPAAAACTAACACCATCTTTGCAAAACCTATATCAGAAATATGTCTGTGTGAGAAATC 733  
 Db 1052 TGATPAAAACTAACACCATCTTTGCAAAACCTATATCAGAAATATGTCTGTGTGAGAAATC 1111  
 OY 734 ATCACTGCGCATCTACAAATTTGGCATGCTTGCAGAAATCAAGGCTTCTGTCTATTTGCCAA 793

Accession	Sequence	Length
Db 1112	ATCACTGGCCATCTACACATTGGGCACTGCTTGAGAAATCAAGGCTTCTTGCTATTTTGCCA	1171
QY 794	AGGAATGACACAGG	808
Db 1172	AGGAATGACGTAG	1186

RESULT 3  
US-07-688-352C-19

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: Sequence 19, Application US/07688352C
: Patent No. 5527896
:
: GENERAL INFORMATION:
:
: APPLICANT: Migler, Michael H.
: APPLICANT: Colicelli, John J.
:
: TITLE OF INVENTION: Cloning By Complementation and Related
: Processes
:
: NUMBER OF SEQUENCES: 57
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murry &
: ADDRESSEE: Ricknell, .
:
: STREET: Two First National Plaza, 20 South Clark
:
: STREET: Street
:
: CITY: Chicago
:
: STATE: Illinois
:
: COUNTRY: USA
:
: ZIP: 60603
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: Patent In Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/07/688,352C

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1  FILING DATE: 19910419
2  CLASSIFICATION: 435
3  PRIOR APPLICATION DATA:
4  APPLICATION NUMBER: US 07/511,715
5  FILING DATE: 20-APR-1990
6  ATTORNEY/AGENT INFORMATION:
7  NAME: Borun, Michael F.
8  REGISTRATION NUMBER: 25447
9  REFERENCE/DOCKET NUMBER: 27805/30197
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (312) 346-5750
12 TELEFAX: (312) 984-9740
13
14 TEXT: 25-3856
15
16 INFORMATION FOR SEQ ID NO: 19:
17
18 SEQUENCE CHARACTERISTICS:
19     LENGTH: 3987 base pairs
20     TYPE: NUCLEIC ACID
21     STRANDEDNESS: single
22     TOPOLOGY: linear
23
24 MOLECULE TYPE: CDNA
25
26 FEATURE:
27
28     NAME/KEY: CDS
29     LOCATION: 3..1498
30
31 US-07-688-352C-19
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OY	198	GAAAAGGTGAAAGACTATTATTAAGCTTTCAAAAGATCTCCCATCGACGAAGCCTCTGG	257
Db	365	AAGGAATATCAGAAGGCTTACTAAGTTTTCCAGCGATATCTTAAGATCTTCACGCTTTTTGC	424
OY	258	TGGAATTATATCACACAAAGCCCCCTCTGCACCTGCTGATGAAGACTACCTTGACAAGCAAG	317
Db	425	TGTAATCTGGGTTTCCAATTTCCTCAAACATTTTAGATGATGATTTAAAGCAAGCCAA	484
OY	318	GCATATCTCTCCCAAATGGGAATGTRGGATTTTTGACATTTTCTGTGTTGATCGCTTGAC	377
Db	485	GTGATCTCTGAAAAAATGTGGAAATGGAAATTTTGATATCTTTCTAATTTGAATGACTAAC	544
OY	378	AAATGGAAACAGCCTGTATACTGTGTTGCCACCCTTCAATPACCATGGACATATCA	437
Db	545	AAATGGAAATAGTCTACTAAGCTTAAOCCTTCAATTATTTAGCTTTCAGATTAATTTGA	604
OY	438	CCATTTCAAGTTAGATATVSGTGAACCTTTACACGAGATTTTATGATGTTCAAGAAGATTA	497
Db	605	GTACTTCATTTAGATATVGTATGAACCTCTGATAACTTTTATGATATGATTTCAAGAAGATTA	664
OY	498	CCACAGCAAAAACCCGATATACAAATGCTGTGTACAGAGCGACGACGACCAAGGCCATGCA	557
Db	665	CCACAGCTAAATATCTTACATTAACGAGATCCAGCTGGGAGATGTACTACAGGCCATATCA	724
OY	558	CTGCTACCTGAAAGAGCCAAAGCTTTGCGACCTTCTCACAGCCTCTGGACATGATCTGG	617
Db	725	CTGTATTCTTAAAGAACCTTAAGCTTGCCAACTTCTGATACCTCTGTGGATATCTGCTGAG	784
OY	618	ACTGCTGGCTGCAGACACACATGTTGGACACCCAGAGGGTGAACCAACCTTTTGTAT	677
Db	785	CTTATTTGCACCTGCCCACATGATATCTGGATCTGATCCAGGGTTTAAACAACCTTTCCTTAT	844
OY	678	AAAAACTRACACCACCATTTCTCAAAACCTATATTCAGATATATGTCTGTGCTGGAAATATCA	737
Db	845	TAAAACTRACCATTTACTTGTGGCAACTTTATRCAGAGATFACCTCAGTACGTGAAAAATCACCA	904
OY	738	CTGGGAGATCTAACAAATTGGCATVGTCTCGAGANTCAAGGCTTCTTGCTCATTTGCCAAAGGA	797
Db	905	CTGGAGATCTGECAGTGGGCTTATTTAGAGNATCAGGCTTATTTCTACATCTCCCTTATGA	964
OY	798	AATGACACAGSATTTTTCACACAGCGTGGGCTTCCTTGATCTTGGCAACAGACATATCAACAG	857
Db	965	AAGCAGCGACAAATVVGAGACACAGATAGGTGCTCTGATACTAGCCACAGACATATGCTG	1024
OY	858	GCAGATATGAATTTTTTGACACGATTTGAAGCTCACCTCCACATTAAGACATTATAGACTGGA	917
Db	1025	CCAGATATAGTATCTGCTTCTTGTGTTAGTCCCATTTGGATAGAGGTGATTTATGCTAGA	1084
OY	918	GGATGCAAGSACAGGCACCTTATGCTTTCAGATCGCCTTGAAGTGTGCTGACATTTGCA	977
Db	1085	AGACACACAGACACAGACATTTGGTTTTTACAGATGAGGTGTTGAATGTGCTGATATTTGTAA	1144
OY	978	TCTTTGTAGATCTGGGAGATGAGCAAGCGTGGAGCTGGAAGAGGCTGTGTAAGATATCTGA	1033
Db	1145	CCCATCTGCGACGTGGGAATTAAGCAACGCACTGTSAGTGAAGAAAGTATACGAGAGAAATCTTT	1204
OY	1038	CAGGCAAGGTGACCTTGACAGAAATTTGAACTGGAATTCAGTCCCTTTTGATCAACA	1097
Db	1205	CCATCAAGGAGATPATPAACAAAAAATATCTATTTGGCTGTGACGACCTTTGGCATGTCCA	1264
OY	1098	GAAGATTTCCATCCCTCTGATATACAAATVTGGTTTCAATGACTCTACATCGTGGAGCGCTGT	1157
Db	1265	CACHTAATCTATTTGCCAACATCCAGATATGTTTTATGACTTCTACTAGTGGAGACTTTTATTT	1324
OY	1158	CCGGAATGGGCCCATTTTCAAGGGTAAACAGACACCCCTGTGGAAGAACATCTGGGCCACT	1217
Db	1325	TACAGAAATGGGCGAGGTTTTTC---CAATACAAAGGCTATCCCAAGACAAATCTCTGGACAGT	1381
OY	1218	CGCACACAAACAAGGCCACAGTGAAGAGGCTGTGTTGCCAGGACAGCACAGAAAGCAGGGGCA	1276
Db	1382	GGGGCTGAAATTAACCCACGCTGGAGGAGGACTGCAGAGAGAACAAGTCCAGCATGATGAGAGCA	1440

RESULT 4  
US-08-474-379C-19  
Sequence 19, Application US/08474379C  
Patent No. 5977305  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED  
TITLE OF INVENTION: PROCESSES  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive/6300 Sears Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,379C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/206,188  
FILING DATE: 01-MAR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,352  
FILING DATE: 19-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 27866/32771  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-0448  
TELEFAX: (312) 474-6300  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3987 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1498  
US-08-474-379C-19

Query Match 37.0%; Score 500.6; DB 2; Length 3987;  
Best Local Similarity 62.9%; Pred. No. 4,6e-139;  
Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

QY 18 TGAGGAGTGGCGGAAATCTGTTGAGAACCCCGATACAGAAATGCCAAATGCTTGCAT 77  
DB 185 TCAGAGGCGTGGAGCTATTTCTTATGACAGTTCGATCAGACTGCAATTATACATTCGTAT 244  
QY 78 GCTGGGAGATATACGACTTAAGGGTCAAGCGGGGTTCTGCTGAACGCCGTGGCTCTTA 137  
DB 245 GCTAGCAATGATACGCTGTAAGAGCCGAGCAGAGATTGGAATCAGAAAGAGAGTCTCA 304  
QY 138 CCCATTCTACTCCCTCTACTTAACTACAGTACAACTACTCAGGGAGATTGGACCAA 197  
DB 305 CCCATATATGATTTCTATTTCCACTCTCAATCTGAATTTGAAGTGTCTGTCTGC 364  
QY 198 GAAAGGTGAAGAGCATTAAGCTTCAAGTACTCTTCATGATCAAGGCTGCTTCG 257

DB 365 AAGGAATATCAGAAGGCTACTAAGTTCCAGCGATATCTAGANTCTTCACGCTTTTCG 424  
QY 258 TGAATATATACCAAGCCCTCTGCACCTGCTGATAGACATCTCTGGACAGAAG 317  
DB 425 TGTACTGCGGTTCAAATTCCTTAACCAATTTAGATGATGATTAATGAGACAGCAA 484  
QY 318 GCATATCTCTCCAAAGTGGGAATGCGGATTTTGACATTTTCTGTTTCTGCTTGC 377  
DB 485 GTGATCTCTGGAAGAAAGTTGGAAATTTGATATATCTTCAATTTGATATACATAC 544  
QY 378 AATGGAACAGCGCTGTAACTGTTGGCCACCTCTGCAATCCATGGAGTACTTCA 437  
DB 545 AATGGAATATGCTAGTAAAGCTTAACCTTTATATTTAGTCTTCATGATTAATTA 604  
QY 438 CCATTTAAGTATGATATGCTGACCTTACACCGATTTTATGATGTTCAAGAAATTA 497  
DB 605 GTACTTCAATTAATGATATGTAAGTCTGTAATTTTATGATGATTCAGAAAGATTA 664  
QY 498 CCACAGCAAAACCCGATACAAATGCTGTTCAGCAGCCGACGTCACCCAGCCATGCA 557  
DB 665 CCACAGTCAAAATCTTACCATACGACGTCAGCTGCGATGTTACTCAGGCCATGCA 724  
QY 558 CTGCTACCTGAAGAGCCAAAGCTTGCCAGCTTCTCAGCGCTCTGACATCATCTTGG 617  
DB 725 CTGTTACTTAAAGAACCTTAAGCTTGCCAAATCTGTAACCTCTGGGATATCTTGAG 784  
QY 618 ACTGCTGGCTGCAGCAGCAGCAGATGAGACCCAGGGGTGAACAGCCATTTTGAT 677  
DB 785 CTTAATTCAGCTGCACATCATGATCTGGATCATCAGGTGTAATCAACCTTCTTAT 844  
QY 678 AAAAATCAACCATCTTGTCAAACTATATAGAAATTTGCTGGCGGAGGAATCTCA 737  
DB 845 TAAATCTAACCATTTACTTGGCAACTTATACAAAGATACCTCAGTACGAGAAATACCA 904  
QY 738 CTGGCAATCTACAAATGAGATGCGATGCGAATCAAGAGGCTTCTGCTCAATTTGCCAAGGA 797  
DB 905 CTGAGATCTGCAGTGGCTTATGAGAAATCAGGCTTATTCACATCTGCCATTTAGA 964  
QY 798 AATGACACAGATATTTGAACAGCAGCTGGCTCTTGTATCTTGGCAACAGATCAACAG 857  
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QY 858 GCAATGAATTTTGTACCAAGATTGAAGCTCCTCCACAAATTAAGACTTAAGACTGGA 917  
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QY 918 GATGCAAGCAGCAGCAGCATTATGCTTCAGATTCCTTGAAGTGTGTCACATTTGCAA 977  
DB 1085 AGACACCCAGACAGACATTTGTTTACAGATGCTTGAAGATGCTGATATTTGTA 1144  
QY 978 TCCATTAGAAATCTGGAGATGAGCAGAGAGTGAAGGCTGTGTAAGAAATCTTA 1037  
DB 1145 CCCATGCGAGCTGGGAATTAAGCAGCAGGAGTGAAGAAAGTAAGGAGGAATCTT 1204  
QY 1038 CAGGCAAGGGAACCTTGAACAGAAATTTGAATGGAATTCCTCTTGTATGATACAA 1097  
DB 1205 CCAATCAAGGAGATATGAAAAAATATCATTTTGGGTGTAGTCCACTTTTGGATGCTCA 1264  
QY 1098 GAAAGATTCATCTCCTAGATATCAAAATGCTTCAATGAGCTACATCTGGAAGCCGCTT 1157  
DB 1265 CACTGATATCTATGCAACATCCAGATTTGGTTTATTTGATACCTAGTGGATTTATTT 1324  
QY 1158 CCGGGAATGGCCCATTTTACGGGTAAAGCAGCCCTGTGAGAAATGCTGGGCCACT 1217  
DB 1325 TACAGATATGGCCAGGTTTTC---CAATTAACAGGCTATATCCCAAGCAATGTGGACAGT 1381  
QY 1218 CGCACACAACAGGCCCAATGGAAGAGCCTGTTGCCAGGACAGCAAGAGAGGGCA 1276  
DB 1382 GGGGCTGAATTAAGACAGCTGGAAGAGAGTCCAGAGAAACAGATGAGAGTGAAGCA 1440

RESULT 5  
US-09-146-249A-19

Sequence 19, Application US/09146249A  
Patent No. 6069240  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Complementation and Related  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,249A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3987 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1498  
US-09-146-249A-19

Query Match 37.0%; Score 500.6; DB 3; Length 3987;  
Best Local Similarity 62.9%; Pred. No. 4.6e-139;  
Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

QY 18 TGAAGGTGGCGAATCTTGTGAGAACCCCGATCAGATGCCAATGTGTTGCAT 77  
DB 185 TCAAGGCGTGAGCTATTCCTATGACAGTTCTGATCAGACTCATATATCATTCGAT 244  
QY 78 GCTGGAGATATAGACTAAGGGGTGACAGCGGGTCTGCTAGACCCCTGGCTCCTCA 137  
DB 245 GCTGAGGATCTACGTGTAAGAGCCGAGCGAGATTGGAATCAGAAAGAGAGTTCTCA 304  
QY 138 CCATTCATCTGCTCGCGCTACTTAACAGTACATCTCAGGGAGATGGCACCAA 197  
DB 305 CCCATATATGATTTTCTGATTTTCCACTCTCATCTGAATCTGAAGTGTCTGTCTGC 364  
QY 198 GAAAGGTGAAAGACTATTAAGCTTTCAAAGTACTTCATGATCAAGGCTGCTCG 257  
DB 365 AAGGAATATCAAGAGCTACTAAGCTTTCACGCGATCTTGAATCTTCACGCTTTTTCG 424  
QY 258 TGAATATATACCAACACCCCTCTGACCTGCTGATGAGACTACCTGGACAAGCAAG 317  
DB 425 TGTATGCGGCTTCAAAATTCCTTAACATTTTATGATGATATATATGACACAAGCAA 484  
QY 318 GCATATGCTCTCCAAAGTGGAGATGGGATTTTGAACATTTCTTGTGATGCGCTTGAC 377  
DB 485 GTGATGCTGTGAAAAGTGGAAATTTGATATTTTGTATTTGATAGACTAAC 544

QY 378 AATGGAACAGCCGTGTAACATGTTGTGCCACCTCTCAATACCATGAGACTATCA 437  
DB 545 AATGGAATATGCTAGTACCTTAACCTTATTTATTTAGTCTTCAATGATTAATGA 604  
QY 438 CCATTTCAAGTTAGATATGAGTACCTTACACCGATTTTACTCATGTTCAAGAGATTA 497  
DB 605 GTACTTCATTTAGATATGATGAACCTCGTAGATTTTACTTATGATATGAAGAATTA 664  
QY 498 CCACAGCCAAAACCCGATATCAATGCTGTTCAGCAGCCGACGTCACCCAGCCATGCA 557  
DB 665 CCACAGTCAAAATCTTACATTAACGACGCTGCGGATGTTACTCAGGCGCATGCA 724  
QY 558 CTGCTACTGTAAGAACCCAAAGCTTCCAGCTTCTCTCAAGCTCTGACATCATGCTGG 617  
DB 725 CTGTACTTAAGAAACCTTAAGCTTGGCAATTCGTATCTCTGGGATATCTTGAG 784  
QY 618 ACTGCTGCTGACAGCAGACAGATGTGACACCCAGGGGTGAACAGCCATTTTGAT 677  
DB 785 CTATATGACAGCTGCACTCATGATCTGTGATCATCCAGGTGTTATCAACCTTCTTAT 844  
QY 678 AAAAATTAACCATCTTGGCAAACTTATATCAGAAATGTCTGTGAGAAATCATCA 737  
DB 845 TAAACTTAACCATTAAGCTTGGCACTTATATCAAGAAATCTCAGTACTGAAATACCA 904  
QY 738 CTGCGATCTCAATTTGGCATGCTTCAGAAATCAAGGCTTCTGCTCATTTGCCAAAGA 797  
DB 905 CTGAGATCTCACTGAGCTTATTTAGAGAAATAGGCTTATCTCACATTCGCATTAGA 964  
QY 798 AATGACAGAGATATTTGAACAGAGCTGGGCTCTTGTGATCTTGGCAACAGATCAACAG 857  
DB 965 AAGCAGCAACAAATGGAGACAGATATGCTGTGATCTGATACCAACAGACATCAGTGC 1024  
QY 858 GCAGATGATTTTGTGACAGATTGAAAGCTCCTCCCAATTAAGACTTAAGCTGGA 917  
DB 1025 CCAGAAATGATATCTGCTTGTAGGTCCCATTTGGATGAGGTGATTTATGCTTGA 1084  
QY 918 GGATGCAACAGGACAGCACTTATGCTTCAGATGAGCTTGAAGTGTGATTTGCA 977  
DB 1085 AGACACAGACAGACATTTTGTTTACAGATGCTTGAAGTGTGATTTGTA 1144  
QY 978 TCTTTGTAGATCTGGAGATGACAGCAGTGAAGGCTCTGTGAAGATTTGA 1037  
DB 1145 CCATATCTGAGCTGTGGATTAACCAAGCAGTGAAGTGAAGATTTGTA 1204  
QY 1038 CAGGCAAGTGAACCTTGAACGAAATTTGAACGTGAATAGCTCTTTGTAATCAACA 1097  
DB 1205 CCATCAAGGAGATATTAAGAAAAATATCATTTGGTGTGATGTCACCTTTCGATCGTCA 1264  
QY 1098 GAAAGATTCATCCCTATATCAAAATGTTTCAATGATGATCAATCTGAGAGCCGCTCT 1157  
DB 1265 CACTGAATCTATTTGCAACATTCAGATTGTTTATGATCTTACCTAGTGAAGCTTAT 1324  
QY 1158 CCGGGAATGGGCCCATTTTACAGGGGTAAACAGCACCTGTGCGAAGAAATGCTGGCCACT 1217  
DB 1325 TACAGAAATGGGCCAGGTTTTC---CAATACAAAGCTATCCCAAAATGCTTGGACAGT 1381  
QY 1218 CGCACACAAACAGCCAGTGAAGAGCTTGTGCCAGGACGACAGACAGAGAGGCA 1276  
DB 1382 GGGGCTGAATTAACCCAGCTGGAAGGAGCTCAGAGAGAAAGTGCAGCTGAGGACA 1440

RESULT 6  
US-08-206-188B-19  
Sequence 19, Application US/08206188B  
Patent No. 6100025  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Complementation and Related  
NUMBER OF SEQUENCES: 84  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/206,188B  
FILING DATE: 01-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3987 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1498  
US-08-206-188B-19

Query Match 37.0%; Score 500.6; DB 3; Length 3987;  
Best Local Similarity 62.9%; Pred. No. 4,66-139;  
Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;  
QY 18 TGAAGAGTGGGAAATCTTTTGAAGACCCCGATAGATGCCAAATGTGTCAT 77  
DB 185 TCAAGAGCGTGGAGCTTCTTCTATGACAGTTCTGATCAGACTGATTAACATTCGTAT 244  
QY 78 GCTGGAGATATACGACTAAGGGCTCAGAGGGGGTTCGCTGAACGCCGTGGCTCTTA 137  
DB 245 GCTAGGAGATGATGCTGTAAAGAGCCGAGCAGGATTTGAATCAGAAAGAGAGGTCTCA 304  
QY 138 CCCATTCATTGACTCCGCTACTTAAGATACATCAATCACTCAGGGAGATTTGGACCAA 197  
DB 305 CCCATTCATTGATTTGATTTGATTTTCCACTCAATCTGAATTAAGTGTCTGTCTGC 364  
QY 198 GAAAAGGTGAAAAGACTTAAAGCTTCAAGATCTTCATCATCAAGGCTGCTGC 257  
DB 365 AAGGAATATACAGAGGCTTAAAGTTCCAGGATATCTTAGATCTTCAGGCTTTTTCG 424  
QY 258 TGAATTAATACCAAGCCCTCTGACCTGCTGATGAAGAACTACCTTGAAGCAAG 317  
DB 425 TGTACTGGGTTTCAAAATCCCTTAACATTTTATGATATATATATGACACCA 464  
QY 318 GCATATGCTCTCAAGAGTGGGAATGTGGATTTTGAATTTCTTCTGTTTGTGCTTGC 377  
DB 485 GTGTATGCTGAAAAGTGGAAATTTGATTTGATTTCTTTTATTTATTTATGACTAAC 544  
QY 378 AAATGAAACAGCTTGTAAACCTGTGTGCACCTCTTCAATACCCATGACTCATCA 437  
DB 545 AAATGAAATATCTAGTAAGCTTAACCTTTCATTTATTTAGTCTTATGATTAATGA 604  
QY 438 CCATTCAGTTAGATATGATGACCTTACACGATTTTATGATGTTTGAAGATTA 497  
DB 605 GTACTTCATTTAGATATGATGAACCTTCGTAGATTTTATGATTAATTCAGAAAGTAA 664

QY 498 CCACAGCCAAAACCCGATATCAATGTCTTTACAGCAGCCGAGCTCACCCAGCCCATCA 557  
DB 665 CCACAGCTAAAATCTTACATTAACGAGTCCAGCTGGGGAGTATACAGCCCATCA 724  
QY 558 CTGCTACCTGAAAAGCAAGCTTGGCCAGCTTCCCTACAGCCCTGAGATCATCTGG 617  
DB 725 CTGTACTTAAAGAACCTTAAGCTTGGCAATCTGTAACTCCCTGGGATATCTCTGAG 784  
QY 618 ACTGCTGCTGACACAGCAGATGTGAGCAGCCAGCCAGGGGGAAGCAAGCCATTTGAT 677  
DB 785 CTATATTCACCTGCACTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 844  
QY 678 AAAAATCAACCACTCTGCAAAACCTATTCAGATATGTGCTGCTGAGCAATCA 737  
DB 845 TAAATCAACCACTTACTTGGCACTTATACAAATTAACCTCACTGATGAAAAATCACCA 904  
QY 738 CTGGGATCTCAATTTGGCATGCTGAGATTAAGCTTCTTCTGCTCATTTGCCAAGA 797  
DB 905 CTGAGATCTCAGTGGCTTATTTAGAGATATGAGCTTATTTCTCATCTGCTCATTTAGA 964  
QY 798 AATGACACAGATATTTGAACAGACCTGGGCTCTTGTATCTTGGCAACAGATCAACAG 857  
DB 965 AAGCAGGCAACAAATGAGAGACAGATAGGTGCTGATATCAAGCAGACAGATCAAGTGC 1024  
QY 858 GCAGAAATATTTTGAACAGATTTGAAGGCTCACCTCCCAATTAAGACTTAAGACTGA 917  
DB 1025 CCAGATGAGATATCTGTTTGTAGTCCCATTTGATTAAGAGGTGATTAATGCTTGA 1084  
QY 918 GGATGACAGGACAGGACCTTATAGCTTCAATGCTGCTGATGAGTGTGCTGATTTGCA 977  
DB 1085 AGACACAGACAGACAGATTTGTTTACAGATAGGTGCTTGAATGCTGATATTTGTA 1144  
QY 978 TCGTTGTAATCTGGAGATGAGCAAGAGAGTGAAGAGTGTGTAAGAAATCTTA 1097  
DB 1145 CCATGCTGAGACCTGGAATTAAGCAAGCAGTGAAGTGAAGAAATGAGAGAGATTTCTT 1204  
QY 1038 CAGCAGGCTGACTTAACAGAAATTTGAACCTGCAATCACTCTTTTGTATCAACA 1097  
DB 1205 CCATGAGGATATGAGAAAAAATATCTATTTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1264  
QY 1098 GAAAGATTCATCTCTATATACAAATTTGATTTGATGACTTACATGCTGAGAGCCGCTCT 1157  
DB 1265 CACTGAATCTATTTGCAACATTCAGATTTGATTTGATGACTTACATGCTGAGAGCCGCTCT 1324  
QY 1158 CCGGAATGGGCCCATTTTCAAGGCTAAGCAACCTCTGCGAAGCAATGCTGGGCCACT 1217  
DB 1325 TACAGAAATGGGCCAGGTTTTC--CAATACAGGCTATCCGAGCAATGCTTGGACAGCT 1381  
QY 1218 CGCAGACAGAAAGCCCGAGGAGAGAGCTGTGCGCAGAGCAGCAGACAGAGAGGCA 1276  
DB 1382 GGGCTGAATTAAGCCAGCTGTAAGGAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440

RESULT 7  
PCT-US91-02714-19  
Sequence 19, Application PC/TUS9102714  
GENERAL INFORMATION:  
APPLICANT: Wiegler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Complementation and Related  
TITLE OF INVENTION: Processes  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/02714  
FILING DATE: 19910419  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25447  
REFERENCE/DOCKET NUMBER: 27805/30197  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3987 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..1498  
PCT-US91-02714-19

Query Match 37.0%; Score 500.6; DB 5; Length 3987;  
Best Local Similarity 62.9%; Pred. No. 4,6e-139;

Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

QY 18 TGAAGAGTGGCGAAATCTGTTTGAAGAACCCGATCAGAAATGCTGTTGCAT 77  
DB 185 TCAGAGCGCTGGAGCTATTCCTATGACAGTCTGATCAGACCTATTATACATTCGTAT 244  
QY 78 GCGGGGAGATATGAGTAAAGGGGTGAGAGGGGTGCGTGCAGAGCGGCTGCTCTCA 137  
DB 245 GCTAGGAGATGATGCTGTAAGAGCGGAGCAGAGATTTGAATCAGAAAGAGGTTCTCA 304  
QY 138 CCCATCATTTGACTTCCGCTACTTAAACATACATACATCAAGGGAGATTTGGACCAA 197  
DB 305 CCCATATATGATTTTCTGATTTTCCACTCTCATCTGAATTTGAATGCTGCTCTGC 364  
QY 198 GAAAAAGTAAAGACTATTAAGCTTTCAAGATCTTCCATGATCAAGAGGCTGCTCG 257  
DB 365 AAGGAATATGAGAGGCTACTAAGTTCCAGCGATATCTTAGATCTTACAGCTTTTTCG 424  
QY 258 TGGAAATATACCAACACCCCTCTGACGCTGCTGATGAGAGCTACTGAGCAAGCAAG 317  
DB 425 TGGAGCTGCGGTTCAAAATTCCTAAACATTTAGATGATGATTAATGAGCAAGCAA 484  
QY 318 GCATATGCTCTCCAAAGTGGGAATGTGGATTTTGCATTTTCTTTGATGCTTGCAC 377  
DB 485 GTGATGCTGGAAGAAATTTGGAATTTGATATCTTCTTATTTGATGATGATGATGAC 544  
QY 378 AATATGAAACAGCTGTGAACACTGTTGCTGACCTTCAATACCATGACTCATTTCA 437  
DB 545 AAAATGGAAAGTCTAGTAAAGCTTAACTTATTTAGTCTTATGATGATGATTAATGA 604  
QY 438 CCATTTCAAGTATGATGAGCTTACACCGATTTTGTGCTATGCTGATGATGATTA 497  
DB 605 GTACTTCAATTTAGATATGATGAACTTTCGAGATTTTATGATGATGATGATGATGAT 664  
QY 498 CCACAGCAAAACCCGATACATGCTGTGTCAGCAGCGAGCTCAACCCAGCCATGCA 557  
DB 665 CCACAGCAAAACCCGATACATGCTGTGTCAGCAGCGAGCTGATGATGATGATGATGATG 724  
QY 558 CTGCTACTGAAAGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 617  
DB 725 CTGTTACTTAAAGGAACTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAG 784

QY 618 ACTGCTGCTGACAGCAGACAGATGTGGACCAACGAGGGGTGAACGCCATTTTGAT 677  
DB 785 CTTATATGACAGCTGCGCCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 844  
QY 678 AAAAATAACCAACCTTGTCAAACTATATGATGATGATGATGATGATGATGATGATGAT 737  
DB 845 TAAATACATACATTTACTTGGCACTTATATGATGATGATGATGATGATGATGATGATGAT 904  
QY 738 CTGGCGATCTCAATTTGGCATGCTTGCAGAAATCAAGGCTTCTGCTATTTGCCAAAGA 797  
DB 905 CTGGAGATCTGCAAGTGGGCTTATGAGAAATCAAGGCTTATTTCCATCTGCTATTTAGA 964  
QY 798 AATACACAGGATATTAACAGACGCTGGGCTCTTATCTGATGATGATGATGATGATGAT 857  
DB 965 AAGCAGCAAAATTTGAGACACAGATGATGATGATGATGATGATGATGATGATGATGATG 1024  
QY 858 GCAGAAATATTTTGAACAGATTTGAAGAGCTCAACCTCCAAATTAAGCTTAAGACTGGA 917  
DB 1025 CCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1084  
QY 918 GATGACAGAGACAGCAGCTTTATGCTTCAAGATGCTTGAAGTGTGCTGACATTTGCAA 977  
DB 1085 AGACACCAAGACAGACATTTGCTTTACAGATGCTTGAAGTGTGCTGATATTTGTA 1144  
QY 978 TCCCTTGAATCTGGAGATGAGCAGAGCTGAGTGAAGAGGCTGCTGAGAAATCTA 1037  
DB 1145 CCAATGTCGAGCTGGAATTAACAGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1204  
QY 1038 CAGCAGAGTGAATCTGAGACAGAAATTTGAATGAACTGGAATGATGCTTCTTGAATCA 1097  
DB 1205 CCATCAAGAGATTTAAGAAAAATATCATTTGGGTGATGATGATGATGATGATGATGATGAT 1264  
QY 1098 GAAAGATTCATCTTGTATGATCAAAATTTGTTTATGATGATGATGATGATGATGATGAT 1157  
DB 1265 CACGAAATCTATTGCCAATCTCAGATTTGTTTATGATGATGATGATGATGATGATGAT 1324  
QY 1158 CCGGGAATGGGCCCATTTACAGGGGTAAACAGACCCCTGCGGAAGAAATGCTGGGCCACT 1217  
DB 1325 TACGAATTTGGGCCAGTTTTC--CAATACAGGCTATCCAGCAATGCTTGAACACGT 1381  
QY 1218 CGCAGACAGAGCCAGTGGAGAGCCTGTTGCCAGGACGACGACAGCAAGAACAGAGGCA 1276  
DB 1382 GGGGCTGAATTAAGCCAGCTGGAAGGAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAG 1440

RESULT 8  
US-07-688-352C-3  
Sequence 3, Application US/07688352C  
Patent No. 5527896  
GENERAL INFORMATION:  
APPLICANT: Wiegler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Complementation and Related  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/688,352C  
FILING DATE: 19910419

Mon Oct 28 10:51:41 2002

us-09-471-459a-6.rni

Page 8

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2158 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1688
US-07-688-352C-3
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Query Match      8.98; Score 120.2; DB 1; Length 2158;
Best Local Similarity 49.2%; Pred. No. 6.9e-26;
Matches 419; Conservative 0; Mismatches 408; Indels 24; Gaps 3;

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  Db 520 TGGGGCTTAAACATCTTCAACGTGGCTGCTACTCCCATTAATGCGGCTCCATCATGCAAC 579
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  Oy 403 TTGTGCCACTCTTCAATACCATGAGCTCATTCACATTTCAAGTTAATATGAGTACC 462
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  Db 580 ATGTACGGCCATTTTCCAGGAAGAGACCTCTTAAGACGTTCATAATTCCTCCGACACC 639
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  Oy 463 TTACACCGATTTTATGATGATGTTCAAGATTTACACAGCCAAACCGGTATACAT 522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 640 TTCTTAACCTTACATGATGATGATTTAGAAAGACATTTCCATTCGATGCGCATCACAC 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Oy 523 GCTGTTCAGCGACGCGACGTCACCGGCGCATGCTGCTACCTGAAACAGCAAGCT 582
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  Db 700 AGCCTGCACGCTGTGACGTGGCGCATCAACGCAAGTCTCTCTACGCCACACTG 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Oy 583 GCCAGTCTCTTCAGCGCTTGACATCATCTTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 642
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  Db 760 GATGCTGTCTTCACAGACCTGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819
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  Oy 643 GTGACCAACCCAGGGTGAACACGCAATTTTATATAAACTAACCACTTTCACAAC 702
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  Db 820 GTTATATCTCTGAGAGCTCCAAATCAAGTTCTCATCAATACAAATTCGCAACTGCTT 879
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  Oy 703 CTATATCAGAATATGTCTGTGCTGGAATATCATCTGCGGATCTCAATTTGGATGCTT 762
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 880 ATGTATATATGACGAATCTGTGCTGGAACCAATCACTGCTGTGGATTTCAAGCTCTT 939
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  Oy 763 CGAGA-----ATCAAGGCTTCTGCATTTTGCCAAAGAAATGACAGATATTGAAC 817
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  Db 940 CAAGAGAACATTTGCGACATCTTTCAGAACTTTACCAAAACAGCAGCACTGAG 999
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  Oy 818 AGCA-GCTGGGCTCTTGATCTTGCAACAGACATCAAGACAGATGAATTTTGGAC 876
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  Db 1000 AAAATGCTGATGACATGCTGTTAGCAATGATGTCCAAAGCAGATGAGCTCTGCT 1059
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  Oy 877 AGATTGAAGCTCACCGCCCATTAAGACTTAA-----GACTGAG 918
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  Db 1060 GACCTTAAAGAGATGAGAAACAAAGAGTGAAGAGCTCGGCTCTCTCTCTGAC 1119
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  Oy 919 GATGACAGAGAGGACACTTATGCTTCAATCGCTTGAATGCTGAGATTTTGCAT 978
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  Db 1120 AACTATACGTACCGATACAGGTCTTCCCAACATGTTACATTTGCGACAGCTGAGCAAC 1179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Oy 979 CTTTGTAGAACTTGGAGATGAGCAAGCAGTGAAGGAGTGTGTAAGAAATTTTAC 1038
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  Db 1180 CCTACCAAGTCTTGGAGTTGTATCGCAATGAGATGATCCATCATGAGAGATTTTTC 1239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Oy 1039 AGCGAAGTGAACCTTGAACAGAAATTTGAACATGAAATCAGTCTCTTTGTAATCAACAG 1098
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 1240 CAACAGGAGAGCAAAAGACGGAGAGGGAATGAGATTAAGCCATGTGTGATTAACAC 1299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Oy 1099 AAGATTTCATCCCTAGTATATACAAATTTGTTTCATGAGCTACATGCGGCTCTTC 1158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 1300 ACAGCTCTGTGAAAAAGTCCAGGTGTGTTTCATGATCATATGTCCATTCATGTGG 1359
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Oy 1159 CGGGAATGGGC 1169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 1360 GAGACTGGGC 1370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 9
US-08-474-379C-3
Sequence 3, Application US/08474379C
Patent No. 5977305
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
City: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2158 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1688
US-08-474-379C-3
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Query Match      8.98; Score 120.2; DB 2; Length 2158;
Best Local Similarity 49.2%; Pred. No. 6.9e-26;
Matches 419; Conservative 0; Mismatches 408; Indels 24; Gaps 3;
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QY 343 TGGGATTTGACATTTCTGTTGATGCGCTGACAAATGGAACAGCCCTGTAACATG 402
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Db 520 TGGGGGCTTAACATCTTCAACGCTGGCTGGTACTCCATATATGCCCCCTCAATGATC 579
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QY 403 TTGTGCCACCTCTTCAATACCATGAGCTCATTCACCATTTCAAGTTAGATGATGACC 462
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Db 580 ATGTACGCCATTTTCCAGAAAGAGACCTTCAAGACGTTTAAATCTCTCCGACACC 639
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QY 463 TTACACCGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 522
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Db 640 TTGTAACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 699
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QY 523 GCTGTCACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 582
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Db 700 AGCGTCAGCGCTCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 759
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QY 583 GCCAGCTTCTTCACGCGCTCTGACATCATGCTTGACGCTGCTGCTGACGACGACGAT 642
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Db 760 GATGCTGTCTTCAACAGACGCGAAATCTGGCTGCGCATTTTTCAGCTGCGCATCATGAT 819
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QY 643 GTGGACACCCAGGGGTGAACACGACATTTTGTATATAAACAACACCATCTTGCACAC 702
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Db 820 GTTGATCATCTCGGAGCTTCCAAATCAGTTCTCATCAATTAACAATTCGGAACCTGCTTG 879
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QY 703 CTATATCAGAAATATGCTGCTGAGAAATCATCACTGGCGGATCTCAATTTGGCATGCTT 752
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Db 880 ATGTATATAGCAATCTGTGCTGGAACCAACATCAGCTGCTGCTGATTCAGGCTCTT 939
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 763 CGAGA-----ATCAGGCTTCTTGTCTCATTTTGGCAAGAAATAGACACAGATATTGAC 817
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Db 940 CAAGAGGAACATTCGACATCTTTCAGAAATCTTACCAAGAAAGACGCCAGACACTCAG 999
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QY 818 AGCA-GCTGGGCTCTTGTATCTTGGCAACGACATCAACAGGAGATGATTTTGGAC 876
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Db 1000 AAATGTGTATGACATGCTGTAGCAACATGATATGTCAGACATGAGCCTCTGCGCT 1059
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QY 877 AGATTAAGCTCAGCTCCCAATTAAGACTTAA-----GACTGAG 918
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Db 1060 GACCTTAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1119
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QY 919 GATGACAGACAGGACATTTATGCTTCAATGCGCTTGAAGTGTGCTGACATTTGCAAT 978
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Db 1120 AACTATATCTGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1179
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QY 979 CCTGTAGATCTGGGAGATGACCAAGCAGTGGAGTGAAGGCTGTGTAAGATTTAC 1038
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1180 CTTACCAAGCTCTTGGAGTTGTATCGGCAATGATGATGATGATGATGATGATGATGAT 1239
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QY 1039 AGGCAAGTGAATCTTGAACAGAAATTTGAACCTGGAATCAGCTCTTTTATTAACAG 1098
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1240 CAACAGGAGACAAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1299
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QY 1099 AAAGATTCATCCCTAGTATACAAATTTGTTTATGATGATGATGATGATGATGATGAT 1158
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Db 1300 ACAGCTTCTGTGAAAGAGTCCAGGTTGTTTCAATGATGATGATGATGATGATGATGAT 1359
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QY 1159 CGGGAATGGC 1169
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Db 1360 GAGACTGGGC 1370
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```

```

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,249A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2158 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1688
; US-09-146-249A-3

Query Match      8.9%; Score 120.2; DB 3; Length 2158;
Best local Similarity 49.2%; Pred. No. 6.9e-26;
Matches 419; Conservative 0; Mismatches 408; Indels 24; Gaps 3;

QY 343 TGGGATTTGACATTTCTGTTGATGCGCTGACAAATGGAACAGCCCTGTAACATG 402
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Db 520 TGGGGGCTTAACATCTTCAACGCTGGCTGGTACTCCATATATGCCCCCTCAATGATC 579
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QY 403 TTGTGCCACCTCTTCAATACCATGAGCTCATTCACCATTTCAAGTTAGATGATGACC 462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 580 ATGTACGCCATTTTCCAGAAAGAGACCTTCAAGACGTTTAAATCTCTCCGACACC 639
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QY 463 TTACACCGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 522
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Db 640 TTGTAACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 699
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QY 523 GCTGTCACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 582
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Db 700 AGCGTCAGCGCTCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 759
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QY 583 GCCAGCTTCTTCACGCGCTCTGACATCATGCTTGACGCTGCTGCTGACGACGACGAT 642
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Db 760 GATGCTGTCTTCAACAGACGCGAAATCTGGCTGCGCATTTTTCAGCTGCGCATCATGAT 819
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QY 643 GTGGACACCCAGGGGTGAACACGACATTTTGTATATAAACAACACCATCTTGCACAC 702
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Db 820 GTTGATCATCTCGGAGCTTCCAAATCAGTTCTCATCAATTAACAATTCGGAACCTGCTTG 879
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QY 703 CTATATCAGAAATATGCTGCTGAGAAATCATCACTGGCGGATCTCAATTTGGCATGCTT 752
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Db 880 ATGTATATAGCAATCTGTGCTGGAACCAACATCAGCTGCTGCTGATTCAGGCTCTT 939
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 763 CGAGA-----ATCAGGCTTCTTGTCTCATTTTGGCAAGAAATAGACACAGATATTGAC 817
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 940 CAAGAGGAACATTCGACATCTTTCAGAAATCTTACCAAGAAAGACGCCAGACACTCAG 999
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QY	818	AGCA-GCTGGGCTCTCTTGATCTTGGCAACAGCATCAACAGGACAGATTAATTTTGGAC	876
Db	1000	AAATGGGATGTGCATGGTGGTTAGCAACTGATATGTCCAGACATCATAGCCTCTGGCT	1059
QY	877	AGATTGAAGCTCACTCCCAATTAAGACTTAA-----GACTGGAG	918
Db	1060	GACCTTAAAGGATGGTAGAAACCAAAAAGGTGACAGCTCCGGTGTCTCTCCTGGAC	1119
QY	919	GATGACAGGACGACGACCTTATGCTTTCAGTCCCTTAAGTGGTGCATCTTGGCAT	978
Db	1120	AAGTATCTGACCGGATATACAGGTTCTTCGGACATGTGCATTTGTGCACCTGAGCAAC	1179
QY	979	CCTTGTAATCTGGGAGATGACACACGATGGAGTGAAGGAGCTGTGCAGAAATTCAC	1038
Db	1180	CTTACACAGTCTTGAGGTTGTATCGGCATGACATGATCGCATATGAGAGAGGTTTTC	1239
QY	1039	AGGCAAGTGAACCTTGAACAGAAATTTGAACGTGGAATATAGTCTCTTTGTATACAG	1098
Db	1240	CACACGGGACAAAGAAACGGGAGAGGGATGGAATTAAGCCATGTGTATTAACAC	1299
QY	1099	AAAGTTTCATCTCTAGTATATACAAATTTGGTTTCATGAGCTACATCGTGGAGCCGCTTTC	1158
Db	1300	ACACCTTCTGTGGAAAGATCCACAGTGTGTTTCATTTGACTACATTGTCTCATCTATTGGG	1359
QY	1159	CGGGAATGGGC	1169
Db	1360	GAGACCTGGGC	1370

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:      NAME/KEY:  CDS
:      LOCATION:  1..1688
US-08-206-188B-3

Query March
Best Local Similarity  8.9%;      Score 120.2;  DB: 3;      Length 2158;
Matches 419;  Conservative  0;  Mismatches 408;  Indels  24;  Gaps  3

```



ATTORNEY/AGENT INFORMATION:  
NAME: CLOUGH, DAVID W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 27866/32771  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-474-379C-80

Query Match 7.8%; Score 105; DB 2; Length 2178;  
Best Local Similarity 47.2%; Pred. No. 2.3e-21;  
Matches 410; Conservative 0; Mismatches 435; Indels 24; Gaps 2;

QY 332 AGTGGGATGTGGATTTGACATTTCTTTGATGCGCTTGACAAATGGAACAGCC 391  
DB 312 AGTGAACAAATGGGCTTTCATTTTCAGAAATAGAGATGTGTGTAACCGGCT 371  
QY 392 TGGTAACAGCTTGTGGACCTCTTCATATCCATGAGACTCATTCACATTTCAAGTTAG 451  
DB 372 TGACTGTATCATGACACACCTTTTTCAGAACGGGATTTTAAACATTTTAAATTC 431  
QY 452 ATATGGTACCTTACACCGATTTTATGTCATGCTTCAGAAAGATTACACAGCCAAAC 511  
DB 432 CAGTAGATACCTTATTAATCATCTTATGACTCTCGAACCATTCCTGCTGATGTGG 491  
QY 512 CGTATCACAATGCTGTTACAGCAGCCGACCTCAACAGGCGATGCACTCTACTGTAAG 571  
DB 492 CCTATCACAAATATCCATGCTGACAGATGTGTCCAGTCTACTGCTATTATCTA 551  
QY 572 AGCCAAAGCTTGCAGCTTCTCAGCAGCTGACATCATGCTTGACGCTGGCTGGAG 631  
DB 552 CACCTGCTTGGAGGCTGTGTGTACATTTTGGAGATTTTCGACGAATTTTGGCAGTG 611  
QY 632 CAGCAGCATGTGGACACCCAGGGGTGAACAGCCATTTTGAATAAACTAACACAGC 691  
DB 612 CAATACATGATGATGATGATGCTGTGTCATCATCAATTTTCATCAATTAACACTCG 671  
QY 692 ATCTTGAACCTATATCAAGAAATGCTGCTGAGAGATGATGCTGCTGCTATACAA 751  
DB 672 AACTTGCCTGATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731  
QY 752 TTGGCATGCTTGCAGATCAAGC-----TTTGTGCTCATTTTGCAGAAAGAAATGAC 805  
DB 732 TTAATTTGCTTGCAGAAAGAAAGCTGACATTTTCCAGAAATTTGACAAAGAAAGAG 791  
QY 806 AGGATATTGAACAGCAGCTGGCTCTTGTATCTTGGCAGACAGATCAACAGCAGAAATG 865  
DB 792 AATCTTGAAGAAATGCTATGATGATGCTTCTTCAACAGATATGCTCAAAACAGATGA 851  
QY 866 AATTTTGAACAGATGAAAGCTACCTCCACATTAAGAAAGCTTGAAG----- 912  
DB 852 ATCTACGCTGATTTGAAGACATATGTTGAATTAAGAAAGTGAACAGCTTGAAGTTTC 911  
QY 913 -----CTGAGAGATGACAGACAGGACATTTATGCTTGAAGATCGGCTTGAAGTTG 967  
DB 912 TTTCTTGTATTAATTAATTCGATAGATGATGATGATGATGATGATGATGATGATG 971  
QY 968 ACATTTGCAATCTTGTAGAAATCTGGAGATGAGCAAGAGATGAGATGAGAAAGGCTCTG 1027  
DB 972 ATCTGAGCAACCCAAACAGCTCTCTGAGCTGACCGCAGAGGAGGAGGAGATTAATGG 1031  
QY 1028 AAGAAATCTACAGCAAGTGAATCTGAACAGAAATTTGAAGTGAAGTGAAGTGAAGT 1087  
DB 1032 AGGAGTTCTTCCGCAAGGAGACCGGAGAGAGAGAGAGAGTGTGAGATTAAGCCCATGT 1091  
QY 1088 GTAATCAACAGAAAGATTCATCCCTAGTATTAACAAATGTTTCATGAGCTACATCTGTG 1147

DB 1092 GTACACAGCACAATGCTTCCGTGGAGAAATCAAGAGTGGCTTCATGACTATATGTTTC 1151  
QY 1148 AGCCGCTTTCGGAATGAGGCCATTTTC 1176  
DB 1152 ATCCCTCTGGAGACATGGGACGACTC 1180

RESULT 14  
US-09-146-249A-80  
Sequence 80, Application US/09146249A  
Patent No. 6069240  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
TITLE OF INVENTION: Cloning by Complementation and Related  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,249A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: CLOUGH, DAVID W.  
REGISTRATION NUMBER: 36,107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TEXT: 25-3856  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-146-249A-80

Query Match 7.8%; Score 105; DB 3; Length 2178;  
Best Local Similarity 47.2%; Pred. No. 2.3e-21;  
Matches 410; Conservative 0; Mismatches 435; Indels 24; Gaps 2;

QY 332 AGTGGGATGTGGATTTGACATTTCTTTGATGCGCTTGACAAATGGAACAGCC 391  
DB 312 AGTGAACAAATGGGCTTTCATTTTCAGAAATAGAGATGTGTGTAACCGGCT 371  
QY 392 TGGTAACAGCTTGTGGACCTCTTCATATCCATGAGACTCATTCACATTTCAAGTTAG 451  
DB 372 TGACTGTATCATGACACACCTTTTTCAGAACGGGATTTTAAACATTTTAAATTC 431  
QY 452 ATATGGTACCTTACACCGATTTTATGTCATGCTTCAAGAAATTAACACAGCCAAAC 511  
DB 432 CAGTAGATACCTTATTAATTAATGATATGATGATGATGATGATGATGATGATG 491  
QY 512 CGTATCACAATGCTGTTACAGCAGCCGACGATCAACAGGCGATGCACTCTACTGTAAG 571  
DB 492 CCTATCACAAATATCCATGCTGACAGATGTGTGCTGCTGCTGCTGCTGCTGCTGCT 551

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OY 572 AGCCAAAGCTTCCAGCTTCTCTACGCGCTTGACATCATGCTTGAGCTGCTGCGAG 631
DB 552 CACCGCTTGGAGGCTGTGTTTACAGATTTGGAGATTTCTTGACCAATTTTGGCAGTG 611
OY 632 CAGCAGCAGATGGAGCACCAGGGGTGAACCCAGCAATTTTGAATAAACTAACACC 691
DB 612 CAATACATGATGATGATCATCTGCTGTGTCATCAATTTCTGATCAATCAAACTGTG 671
OY 692 ATCTGCAACCACTATATGASATATGCTGTGCTGAGCAATCATGCGGCGATACAA 751
DB 672 AACTGCGCTTGATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
OY 752 TTGGCATCTTCCAGCAATCAAGC-----TTCTTGTCTATTTGGCAAGCAATGAGAC 805
DB 732 TTAATTTCTTCCAGCAAAACCTGTCATTTTCCAGATTTTGACCAAAACCAAGAC 791
OY 806 AGGATATTTGAACAGCAGCTGGGCTCTCTGATCTTGCAACAGACATCAACAGCAAG 865
DB 792 AATCTTTAAGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 851
OY 866 AATTTTGAACAGATTTGAAGCTCAGCTCCAGCAATTAAGACTTAAG----- 912
DB 852 ATCTACTGCTGATTTGAAGACTATGTTGAATAAGAAAGTGAACAGCTCTGAGTTTC 911
OY 913 -----CTGGAGGATGACAGCAGCAGCAGCTTATGCTTCCAGATGCGCTTGAAGTGTG 967
DB 912 TTCTTCTGATATATTTATTCCTGATGATGATGATGATGATGATGATGATGATGATG 971
OY 968 ACATTTGCAATCTTGTGAATCTGGAGATGAGCAAGCAGCAGTGAAGAGTCTGTG 1027
DB 972 ATCTGACCAACCAAGCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031
OY 1028 AAGATTTTACAGGAGAGTGAATTTGAACAGAAATTTGAACTGCAATCTCTCTT 1087
DB 1032 AGGATTTCTTCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1091
OY 1088 GTAATCAACAGAAAGATTCATCTCTGATATCAATTTGTTGATGATGATGATGATG 1147
DB 1092 GTGACACACATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1151
OY 1148 AGCGCTCTTCCGAGAGATGGGCCATTTTC 1176
DB 1152 ATCCCTCTGGAGACATGGCAGACCTTC 1180

- RESULT 15
US-08-206-188B-80
; Sequence 80, Application US/08206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Migler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715

```

```

; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
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; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2178 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-206-188B-80

Query Match      7.8%; Score 105; DB 3; Length 2178;
Best Local Similarity 47.2%; Pred. No. 2,3e-21;
Matches 410; Conservative 0; Mismatches 435; Indels 24; Gaps 2;

OY 332 AAGTGGAAATGGGATTTTGAATTTCTGTTGATGCTTGACAAATGGAACAGCC 391
DB 312 ATGTGACAAATGGGGCTCTCATGTTTTCAGAAATGACAGAGTTGCTGTAACGGCCCT 371
OY 392 TGTGTAACAGCTGTGGCCACCTTCAATACCATGAGCTATTACCATTTCAAGTTAG 451
DB 372 TGACTGTTATATGACACCATTTTTCAGGAACGGGATTTTAAATTAATTAATTC 431
OY 452 ATATGATGACCTTACACCATTTTATGATGATGATGATGATGATGATGATGATGATG 511
DB 432 CAGTATGATCTTTAATTTATATCTTATGATCTCTGGAAGACATTTACATGCTGATG 491
OY 512 CGTATCAACATGCTGTTCACGACCGAGCTGACCCAGGCAATGCACTGCTACTGGAAG 571
DB 492 CCTATCAACAAATATTCATGCTGATGATGATGATGATGATGATGATGATGATGATG 551
OY 572 AGCCAAAGCTTCCGAGCTCTCTCAAGCCCTGAGATCATGCTGTGAGCTGGCTGAG 631
DB 552 CACCTGCTTTGGAGGCTGTGTTTACAGATTTGGAATTTCTGACCAATTTTGGCAGTG 611
OY 632 CAGCAGCAGATGGAGCACCAGGGGTGAACCCAGCAATTTTGAATAAACTAACACC 691
DB 612 CAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 671
OY 692 ATCTGCAACCTATATGAGAAATATGCTGTGCTGAGAGATCATGCTGGCATCTACAA 751
DB 672 AACTTGCCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 731
OY 752 TTGGCATCTTCCAGCAATCAAGC-----TTCTTGTCTCATTTGCCAAAGAAATGAGAC 805
DB 732 TTAATTTCTTCCAGCAAAACCTGTCATTTTCCAGAAATTTGACCAAAACCAAGAC 791
OY 806 AGGATATTTGAACAGCAGCTGGGCTCTCTGATCTTGCAACAGACATCAACAGCAGATG 865
DB 792 AATCTTTAAGAAATGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 851
OY 866 AATTTTGAACAGATTTGAAGCTCAGCTCCAGCAATTAAGACTTAAG----- 912
DB 852 ATCTACTGCTGATTTGAAGACTATGTTGAATAAGTGAACAGCTCTGAGTTTC 911
OY 913 -----CTGGAGGATGACAGCAGCAGCAGCTTATGCTTCCAGATGCGCTTGAAGTGTG 967
DB 912 TTCTTCTGATATATTTATTCGATGATGATGATGATGATGATGATGATGATGATGATG 971
OY 968 ACATTTGCAATCTTGTGAATCTGGAGATGAGCAAGCAGTGAAGAGGCTCTGTG 1027
DB 972 ATCTGACCAACCAAGAGCTCTCCAGCTGTACCGCAGTGAAGAGAGAGAGAGAGAG 1031
OY 1028 AAGATTTTACAGGAGAGTGAATTTGAACAGAAATTTGAACTGCAATCTCTCTT 1087
DB 1032 AGGATTTCTTCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1091

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QY 1088 GTATCAACAGAAAGATTCCATCCCTAGTATACAAATTGGTTTCATGAGCTACATCGTGG 1147  
Db 1092 GTGACACAGCACATGCTTCCGTGAAAAATCACAGGTGGGCTTCATAGACTATATATGTTTC 1151  
QY 1148 AGCCGCTCTTCCGGGAATGGGCCCATTTTC 1176  
Db 1152 ATCCCTCTGGGAGACATGGGCAGACTC 1180

Search completed: October 27, 2002, 07:23:28  
Job time : 76 secs